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OM protein - protein search, using sw model

Run on: August 27, 2004, 20:55:20 ; Search time 23 Seconds

(without alignments)
445,992 Million cell updates/sec

Title: US-09-626-219-1

Perfect score: 1133

Sequence: 1 SQPQAVPPYASNTCRDQF.....QSDTCKNPLEPPEPMSGT 197

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133	100.0	435	1	TNR3_HUMAN
2	771	68.0	415	1	TNR3_MOUSE
3	305	26.9	461	1	TR1B_HUMAN
4	295	26.0	474	1	TR1B_MOUSE
5	285.5	25.2	300	1	TR6B_HUMAN
6	283	25.0	625	1	TR1L_MOUSE
7	278	24.5	277	1	TNR5_HUMAN
8	277	24.4	616	1	TR1L_HUMAN
9	251.5	22.2	269	1	TNR5_BOVIN
10	243.5	21.5	289	1	TNR5_MOUSE
11	242.5	21.4	401	1	TR1B_MOUSE
12	239.5	21.1	401	1	TR1B_HUMAN
13	235.5	20.8	401	1	TR1B_MOUSE
14	230.5	20.3	283	1	TR14_HUMAN
15	228.5	20.2	655	1	TR21_HUMAN
16	226.5	20.0	655	1	TR21_MOUSE
17	225	19.9	349	1	CRMB_CAMPS
18	222.5	19.6	271	1	TNR4_RAT
19	214.5	18.9	272	1	TNR4_MOUSE
20	210.5	18.6	455	1	TR14_HUMAN
21	210	18.5	349	1	CRMB_VARV
22	207	18.3	351	1	CRMB_COMPX
23	206	18.2	461	1	TR1A_PIG
24	203	17.9	323	1	TNR6_BOVIN
25	201	17.7	277	1	TNR4_HUMAN
26	201	17.3	454	1	TR1A_MOUSE
27	196	17.3	595	1	TNR8_HUMAN
28	195.5	17.3	255	1	TNR9_HUMAN
29	194	17.1	332	1	TNR6_PIG
30	189	16.7	325	1	TR7_SIVKA
31	188	16.6	471	1	TR1A_BOVIN
32	184.5	16.3	461	1	TR1A_RAT
33	183.5	16.2	326	1	TR2_MYXVL

34	182	16.1	498	1	TNR8_MOUSE	Q60846 mus musculus
35	181	16.0	335	1	TNR6_HUMAN	P25445 homo sapien
36	179.5	15.8	256	1	TNR9_MOUSE	P20334 mus musculus
37	171.5	15.1	425	1	TR16_RAT	P07174 rattus norv
38	167.5	14.8	440	1	TR10B_HUMAN	O14763 homo sapien
39	166	14.7	493	1	TNR8_RAT	P97525 rattus norv
40	164	14.5	416	1	TR16_CHICK	P18519 gallus gall
41	162	14.3	327	1	TNR6_MOUSE	P25446 mus musculus
42	152.5	13.5	417	1	TR16_MOUSE	Q920W1 mus musculus
43	148.5	13.1	427	1	TR16_HUMAN	P08138 homo sapien
44	145.5	12.8	324	1	TNR6_RAT	Q63199 rattus norv
45	145	12.8	198	1	TR22_MOUSE	Q96r62 mus musculus

ALIGNMENTS

RESULT 1

ID	TNR3_HUMAN	STANDARD;	PRT;	435 AA.
AC	P36941;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 3 precursor			
DE	(lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related protein)			
GN	LTBR OR TNFRSF3 OR TNFR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=93252381; PubMed=8486360;			
RA	Baens M., Chaffanet M., Cassiman J., den Berghe H., Marynen P.,			
RT	"Construction and evaluation of a hncDNA library of human 12p			
RT	transcribed sequences derived from a somatic cell hybrid."			
RL	Genomics 16:214-218 (1993).			
RC	SEQUENCE FROM N.A.			
RX	TISSUE=Lung;			
RA	MEDLINE=22388257; PubMed=12477932;			
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,			
RA	Villalón D., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Fahy J., Heltan E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,			
RA	Butterfield J.S., Schein J.E., Jones S.J.M., Skalska U., Smalls D.E.,			
RA	Schneher A., Schein J.E., Jones S.J.M., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RP	[3]			
RC	FUNCTION.			
RX	MEDLINE=94225209; PubMed=8171323;			
RA	Crowe P.D., VanArsdale T.L., Walter B.N., Ware C.F., Hession C.,			
RA	Ehrenfelds B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.,			
RT	"A lymphotoxin-beta-specific receptor."			
RL	Science 264:707-710 (1994).			
RP	[4]			
RC	CHARACTERIZATION.			

RA MEDLINE=99223511; PubMed=10207006;
 RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
 RA "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
 RT death in HeLa cells";
 RL J. Biol. Chem. 274:11868-11873(1999).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=20261554; PubMed=10799510;
 RA Rooney J.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
 RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
 RT "The lymphotoxin-beta receptor is necessary and sufficient for
 RT LIGHT-mediated apoptosis of tumor cells";
 RL J. Biol. Chem. 275:14307-14315(2000).
 RN [6]
 RP INTERACTION WITH TRAF3.
 RX MEDLINE=96278943; PubMed=8663299;
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
 RA Yagita H., Okumura K.; NF-kappaB and putative signal transducer for
 RT the lymphotoxin-beta receptor";
 RL J. Biol. Chem. 271:14661-14664(1996).
 RN [7]
 RP INTERACTION WITH TRAF4.
 RX MEDLINE=98289299; PubMed=9626059;
 RA Krajewska M., Krajewski S., Zapata J.M., Vanarsdale T.,
 RA Gascoyne R.D., Berern K., McFadden D., Shadalk A., Hugh J.,
 RA Reynolds A., Cleverger C.V., Reed J.C.;
 RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
 RT adult, fetal, and tumor tissues";
 RL Am. J. Pathol. 152:1549-1561(1998).
 RN [8]
 RP INTERACTION WITH TRAF5.
 RX MEDLINE=98172745; PubMed=9511754;
 RA Minushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
 RA Otsuka M., Yamamoto T., Inoue J.-I.;
 RT "Cloning and characterization of a cDNA encoding the human homolog of
 RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";
 RL Gene 207:135-140(1998).
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTR and LTR, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF5. May play a role in the development of lymphoid organs.
 CC -1- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
 CC -1- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
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 CC -----
 CC EMBL: L04270; AAA36757.1; -
 DR EMBL: EC026262; AAH26262.1; -
 DR PIR: I54182; I54182.
 DR HSSP: P25942; 1CDF.
 DR Genem: HGNC:6718; LTR.
 DR MIM: 600979; -
 DR GO: 0007165; P:signal transduction; TAS.
 DR InterPro: IPR008063; Fas_receptor.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PFO0020; TNFR_c6; 4.
 DR PRINTS: PRO1680; FASRECEPTOR.
 DR SMART: SM00208; TNFR_4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00650; TNFR_NGFR_2; 3.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT CHAIN 1 30 POTENTIAL.
 FT SIGNAL 31 435 TUMOR NECROSIS FACTOR RECEPTOR
 FT CHAIN 31 435 SUPERFAMILY MEMBER 3.
 FT DOMAIN 31 227 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 228 248 POTENTIAL.

FT DOMAIN 249 435 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 42 81 TNFR-CYS 1.
 FT REPEAT 82 124 TNFR-CYS 2.
 FT REPEAT 125 168 TNFR-CYS 3.
 FT REPEAT 169 211 TNFR-CYS 4.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 80 BY SIMILARITY.
 FT DISULFID 83 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 104 124 BY SIMILARITY.
 FT DISULFID 126 132 BY SIMILARITY.
 FT DISULFID 139 148 BY SIMILARITY.
 FT DISULFID 142 167 BY SIMILARITY.
 FT DISULFID 170 185 BY SIMILARITY.
 FT CARBOHYD 40 40 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 435 AA; 46709 MW; 6246268022F656F CRC64;
 Query Match 100.0%; Score 1133; DB 1; Length 435;
 Best Local Similarity 100.0%; Pred. No. 9, 1e-90;
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGPQAVPPVASENQTCRDEKEYEPQHRICGRCRPGTVSAKCSIRDTVCATCENS 60
 DB 28 SGPQAVPPVASENQTCRDEKEYEPQHRICGRCRPGTVSAKCSIRDTVCATCENS 87
 QY 61 YNHWNVLTICQCRPCDPVWGLEIAPCTSKRTQCRGCPGFCAMALECTHCELLSD 120
 DB 88 YNEHWNVLTICQCRPCDPVWGLEIAPCTSKRTQCRGCPGFCAMALECTHCELLSD 147
 QY 121 CPPGTEALEKDEYGVKGNHCVCPCAGHFONTSPSARCOPTHRCENGLVEAAGTQSD 180
 DB 148 CPPGTEALEKDEYGVKGNHCVCPCAGHFONTSPSARCOPTHRCENGLVEAAGTQSD 207
 QY 181 TTCNPLEPLPPENSGT 197
 DB 208 TTCNPLEPLPPENSGT 224
 RESULT 2
 ID TNR3 MOUSE STANDARD. PRT; 415 AA.
 AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (lymphotoxin-beta receptor).
 DE LTR OR TNFRSF3 OR TNFCR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 OK (1)
 RN RN
 RP SEQUENCE FROM N.A.
 RP STRAIN=CVB; TISSUE=Lung;
 RC MEDLINE=96072804; PubMed=7594541;
 RX Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RA "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 RT and expression.";
 RT J. Immunol. 155:5280-5288(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=96163885; PubMed=8586432;
 RA Nakamura T., Tashiro K., Nakazawa M., Nakano T., Sasayama S.,
 RA Honjo T.;
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 RT sequence trap and chromosomal mapping.";
 RL Genomics 30:312-319(1995).
 RN [3]
 RP INTERACTION WITH TRAF5.

RC STRAIN=BALE/c;
 RX MEDLINE=96278943; PubMed=8663299;
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
 RA Yagita H., Okumura K.;
 RT "TRAFs, an activator of NF-kappaB and putative signal transducer for
 RT the lymphotoxin-beta receptor.";
 RL J. Biol. Chem. 271:14661-14664(1996).
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and LTb, and for TNFRS14/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF5. May play a role in the development of lymphoid organs
 CC (By similarity).
 CC -1- SUBUNIT: Self-associates (By similarity). Associates with TRAFs.
 CC Associates with TRAF3 and TRAF4 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
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CC -----
 DR EMBL; U29173; AAA68964.1; -;
 DR EMBL; L38423; AAB00846.1; -;
 DR EMBL; U30798; AAA81334.1; -;
 DR HSSP; 014763; 1D0G.
 DR MGD; MG1104875; LdbT.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00505; TNFR_NGFR_2; 3.
 KM Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 415
 FT FT
 FT FT
 FT DOMAIN 31 223
 FT DOMAIN 224 244
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 170
 FT REPEAT 171 213
 FT DISULFID 43 58
 FT DISULFID 59 72
 FT DISULFID 73 80
 FT DISULFID 83 98
 FT DISULFID 101 116
 FT DISULFID 104 124
 FT DISULFID 126 132
 FT DISULFID 139 150
 FT DISULFID 142 169
 FT DISULFID 172 187
 FT CARBOHYD 40 40
 FT CARBOHYD 179 179
 SQ SEQUENCE 415 AA, 44956 MW, 298326A56AE661 CRC64;
 Query Match 68.0%; Score 771; DB 1; Length 415;
 Best Local Similarity 70.7%; Pred. No. 7.1e-59;
 Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SOPQAVPYASNGTCRDOEKYEPQHRICSCRPFGYTSAKSRIIDYCATCAENS 60
 Db 28 SOPQAVPYRIENQTCWQDQKXYEPHMDVCCSRCPGPFVAVCSRSQDITVCKCPHNS 87
 QY 61 YNEHNHYLTICOLGCPDVPWGLERLACTSKTKQCQCPQPMFCAVAALACTHC-ELL 118
 Db 88 YNEHNHNLSTCOLGCPDVLVGLFEVAPCTSRKACRCQCPQMSCVYLDNECVCHCEERL 147
 QY 119 SDQPGTEALEKDEVGKNNHCVPCKAGHFONTSSPASCOPHTCENQGLVEAAPGTQ 178

Db 148 VLCPGTEAETDEIMDVNCPCKPQHFQNTSSPARCQPHTRCEIQGLVEAAPTSTY 207
 QY 179 SDTCKKQPLEP 189
 Db 208 SDTCKKQPLEP 218

RESULT 3
 ID TRIB HUMAN STANDARD; PRT; 461 AA.
 AC P20333; Q16042; Q9UIH1.
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor
 DE necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Etanercept)
 GN [contains: tumor necrosis factor binding protein 2 (TBP2)].
 OS TNFRSF1B OR TNFR2 OR TNFR.
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90260639; PubMed=2160731;
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
 RA Dower S.K., Cosman D., Goodwin R.G.;
 RT "A receptor for tumor necrosis factor defines an unusual family of
 RT cellular and viral proteins.";
 RL Science 248:1019-1023(1990).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT ARG-196.
 RX MEDLINE=91045991; PubMed=2172983;
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
 RA Hale K.K., Squire C.H., Thompson R.C., Vannice J.L.;
 RT "A second tumor necrosis factor receptor gene product can shed a
 RT naturally occurring tumor necrosis factor inhibitor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96299745; PubMed=8661109;
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
 RA Lepelletier D., Stallard B.J., Goeddel D.V., Desautels F.J.;
 RA Brodeur G.M.;
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";
 RL Genomics 35:94-100(1996).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS ARG-196; LYS-232; PRO-269 AND
 RP ARG-301.
 RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Wiltrak L.A., Nickerson D.A.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PNS;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stabileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Utsin T.B., Toshitoki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettleman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,

RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 37-461 FROM N.A.
RX MEDLINE=91370690; PubMed=196549;
RA Dembic Z., Joetscher H., Gubler U., Pan Y.C., Lahm H.-W., Gentz R.,
RA Brochhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RT intracellular, domain sequences.";
RL Cytokine 2:231-237(1990).
RN [7]
RP SEQUENCE OF 116-461 FROM N.A., PARTIAL SEQUENCE, AND VARIANT ARG-196.
RX MEDLINE=90349572; PubMed=2166946;
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RT and demonstration of a shed form of the receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN [8]
RP SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.
RX MEDLINE=21069356; PubMed=1197692;
RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;
RT "New single nucleotide polymorphisms in the coding region of human
RT TNFR2: association with systemic lupus erythematosus.";
RL Genes Immun. 1:501-503(2000).
RN [9]
RP SEQUENCE OF 27-31.
RX MEDLINE=90110215; PubMed=2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors.";
RL J. Biol. Chem. 265:1531-1536(1990).
RN [10]
RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-352.
RX MEDLINE=91056048; PubMed=2173696;
RA Joetscher H., Schläeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA Brochhaus M.;
RT "Purification and partial amino acid sequence analysis of two
RT distinct tumor necrosis factor receptors from HL60 cells.";
RL J. Biol. Chem. 265:20131-20138(1990).
RN [11]
RP CHARACTERIZATION.
RX MEDLINE=93016040; PubMed=1328224;
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA Lipari M.T., Goeddel D.V.;
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT Characterization of ligand binding, internalization, and receptor
RT phosphorylation.";
RL J. Biol. Chem. 267:21172-21178(1992).
RN [12]
RP INTERACTION WITH TRAF2.
RX MEDLINE=94349371; PubMed=8069916;
RA Rothe W., Wong S.C., Henzel W.U., Goeddel D.V.;
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL Cell 78:681-692(1994).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
RP TRAF2.
RX MEDLINE=99221490; PubMed=10206649;
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;
RT "Structural basis for self-association and receptor recognition of
RT human TRAF2.";
RL Nature 398:533-538(1999).
RN [14]
RP VARIANTS ARG-196 AND LYS-232.
RX MEDLINE=21603988; PubMed=11762942;
RA Morita C., Horuchi T., Tsukamoto H., Hatna N., Kikuchi Y.,
RA Arinobu Y., Otsuka T., Sawabe T., Harashina S., Nagasawa K., Niho Y.;
RT "Association of tumor necrosis factor receptor type II polymorphism

RT 196R with systemic lupus erythematosus in the Japanese: molecular and
RT functional analysis.";
RL Arthritis Rheum. 44:2819-2827(2001).
RN [15]
RP VARIANT ARG-196.
RX MEDLINE=22151311; PubMed=12161545;
RA Peral B., San Millan J.L., Castello R., Moghetti P.,
RA Escobar-Morreale H.F.;
RT "Comment: the methionine 196 arginine polymorphism in exon 6 of the
RT TNF receptor 2 gene (TNFRSF1B) is associated with the polycystic
RT ovary syndrome and hyperandrogenism.";
RL J. Clin. Endocrinol. Metab. 87:3977-3983(2002).
RN [16]
RP FUNCTION: Receptor with high affinity for homotrimeric
RX approximately 5-fold lower affinity for heterotrimeric
CC TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the
CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2. The TNF
CC receptor 2 mediates most of the metabolic effects of TNF-alpha.
CC [17]
RP SUBUNIT: Binds to TRAF2.
CC [18]
RP SUBCELLULAR LOCATION: Type 1 membrane protein and secreted.
CC [19]
RP PTM: Phosphorylated; mainly on serine residues and with a very low
CC level on threonine residues.
CC [20]
RP PTM: A soluble form (tumor necrosis factor binding protein 2) is
CC produced from the membrane form by proteolytic processing.
CC [21]
RP PHARMACOLOGICAL: Available under the name Enbrel (Immunex and
CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid
CC arthritis (RA). Enbrel consist of the extracellular ligand-binding
CC portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to
CC TNF-alpha and blocks its interactions with receptors.
CC [22]
RP SIMILARITY: Contains 4 TNFR-Cys repeats.
CC [23]
RP DATABASE: NAME=PROT; NOTE=CD guide CD120b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm";
CC [24]
RP DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
CC WWW="http://www.enbrel.com/".
CC [25]
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CC -----
DR EMBL; M32315; AA559829.1; -;
DR EMBL; U52165; AAC50622.1; -;
DR EMBL; U52156; AAC50622.1; JOINED.
DR EMBL; U52157; AAC50622.1; JOINED.
DR EMBL; U52158; AAC50622.1; JOINED.
DR EMBL; U52159; AAC50622.1; JOINED.
DR EMBL; U52160; AAC50622.1; JOINED.
DR EMBL; U52161; AAC50622.1; JOINED.
DR EMBL; U52162; AAC50622.1; JOINED.
DR EMBL; U52163; AAC50622.1; JOINED.
DR EMBL; U52164; AAC50622.1; JOINED.
DR EMBL; M55994; AAA36755.1; -;
DR EMBL; AY264804; AA089076.1; -;
DR EMBL; AY264804; AAP88939.1; -;
DR EMBL; BC052977; AAH52977.1; -;
DR EMBL; S63368; AAB19824.2; -;
DR EMBL; M35857; AAA63262.1; -;
DR EMBL; AB030950; BAA89053.1; -;
DR PIR; A35356; A35356.
DR PDB; 1CA9; 12-APR-99.
DR Genew; HGNC:11917; TNFRSF1B.

Query Match 26.9%; Score 305; DB 1; Length 461;
Best Local Similarity 35.0%; Pred. No. 4.9e-19;
Matches 70; Conservative 24; Mismatches 76; Indels 28; Gaps 9;
QY 5 APPVASE-NOTCRDEKEYEPQHRICCSROPPEGYTVAKSRSIRDTYCATCAENSYNE 63
DB 28 ALTPVAPBPGSTCR--LRFYDQTAQCCSKSPGQHAUVFCTKTDYVSCDSBSTYTO 85
QY 64 HNNYLTICQLCR---PCDEVMGLIELIAPCTSRKTKQCRQPGMFCAMALE-CTHCELLS 119

RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal lung;
 RA MEDLINE=99087326; PubMed=9872321;
 RA Pilti R.M., Martens S.A., Lawrence D.A., Roy M., Kischkel F.C.,
 RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
 RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
 RA Goddard A.D., Botstein D., Ashkenazi A.,
 RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
 RT colon cancer.";
 RL Nature 396:699-703(1998).
 [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
 RC TISSUE=Prostate;
 RA MEDLINE=99253915; PubMed=10318773;
 RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
 RT "A newly identified member of tumor necrosis factor receptor
 RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
 RL J. Biol. Chem. 274:13733-13736(1999).
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA MEDLINE=20122600; PubMed=10655513;
 RA Bai C., Connolly B., Metzger M.L., Hilliard C.A., Liu X., Sandig V.,
 RA Soderman A., Galloway S.M., Liu O., Austin C.P., Caskey C.T.;
 RT "Overexpression of M68/Dc3 in human gastrointestinal tract tumors
 RT independent of gene amplification and its location in a four-gene
 RT cluster.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
 [4]
 RP SEQUENCE FROM N.A.
 RA Matthews L.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung, and Skin;
 RA MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hopkins R.F., Zeeberg B., Buetow K.H., Scheeler C.F., Bhat N.K.,
 RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stachenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.R.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Cantini P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulys S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scheraga A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RP FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF4/LIGHT
 and TNFSF6/FasL. Protects against apoptosis.
 [7]
 RP SUBCELLULAR LOCATION: Secreted.
 [8]
 RP TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
 Detected in adult stomach, spinal cord, lymph node, trachea,
 spleen, colon and lung. Highly expressed in several primary tumors
 from colon, stomach, rectum, esophagus and in SW480 colon
 carcinoma cells.
 [9]
 RP SIMILARITY: Contains 4 TNFR-Cys repeats.
 [10]
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CC -----
 DR EMBL: AF104419; AAD03056.1; -
 DR EMBL: AF134240; AAD29688.1; -
 DR EMBL: AF217796; AAF35244.1; -
 DR EMBL: AF217793; AAF33685.1; -
 DR EMBL: AF217794; AAF33686.1; -
 DR EMBL: AL121845; CAC03668.1; -
 DR EMBL: BC017065; AAI17065.1; -
 DR EMBL: BC034349; AAI17065.1; -
 DR HSSP: O14763; 1D0G; -
 DR Genew; HGNC:11921; TNFRSF6B.
 DR MIM; 603361; -
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0006916; P:anti-apoptosis; TAS.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 4.
 DR SMART; SM00208; TNFR; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 DR Receptor; Apoptosis; Glycoprotein; Repeat; Signal.
 KM SIGNAL 1 29
 FT CHAIN 30 300
 FT REPEAT 31 70 TUMOR NECROSIS FACTOR RECEPTOR
 FT REPEAT 72 113 SUPERFAMILY MEMBER 6B.
 FT REPEAT 115 150 TNFR-CYS 2.
 FT REPEAT 152 193 TNFR-CYS 3.
 FT REPEAT 195 232 TNFR-CYS 4.
 FT DISULFID 49 62 BY SIMILARITY.
 FT DISULFID 52 70 BY SIMILARITY.
 FT DISULFID 73 88 BY SIMILARITY.
 FT DISULFID 91 105 BY SIMILARITY.
 FT DISULFID 95 113 BY SIMILARITY.
 FT DISULFID 115 126 BY SIMILARITY.
 FT DISULFID 132 150 BY SIMILARITY.
 FT DISULFID 153 168 BY SIMILARITY.
 FT DISULFID 174 193 BY SIMILARITY.
 FT CARBOHYD 173 173 N-LINKED GLCNAC... (POTENTIAL).
 SQ SEQUENCE 300 AA; 32679 MW; P90AE33718449AF CRC64;
 Query Match 25.2%; Score 285.5; DB 1; Length 300;
 Best Local Similarity 36.0%; Pred. No. 1.5e-17;
 Matches 63; Conservative 18; Mismatches 77; Indels 17; Gaps 7;
 QY 25 EPQRICRCRPPGGVYASXSRIRDTVCATCAENSYEHNNVYLITCOLCEPCDPVMG-- 82
 DB 42 EGERLVCAQCPGTFVORPCRDSPITCGPCPPHYQFMYL---ERCRYNVLCGER 98
 QY 83 LEEIAPCTSKRKTQRCQCPGMFC-AAMALCTCHCLSDCPGTEAEIKDEVGKNNHCV 141
 DB 99 EEEAACHATNHRACRGTGFVAHAGFLE--H---ASCPPGA-GVIAPTPSQNTQCO 151
 QY 142 PCKAGHPONTSPSPARCCPHRCENQGLVEAPGTRQSDTQKN---PLEPLPP 192
 DB 152 PCPPPTFSASSSSBQCQPHRNTALGLALNVPGSSSHDTLCTSGTGPLSTRVP 206
 RESULT 6
 TRIL MOUSE STANDARD; PRT; 625 AA.
 ID TRIL MOUSE
 AC 035305; Q8VCT7;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11A precursor
 DE (Receptor activator of NF-kB) (Osteoclast differentiation factor
 DE Receptor) (ODFR).
 GN TNFRSF11A OR RANK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;

[1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Fetal liver;
 RC MEDLINE=96032977; PubMed=9367155;
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Douglall W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
 RA Gilbert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=22386257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrincci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=99097247; PubMed=9876548;
 RA Nakagawa N., Kinoshita K., Yamaguchi K., Shima N., Yasuda H., Yano K.,
 RA Morinaga T., Higashio K.;
 RT "RANK is the essential signaling receptor for osteoclast
 RT differentiation factor in osteoclastogenesis.";
 RL Biochem. Biophys. Res. Commun. 253:395-400 (1998).
 CC -1- FUNCTION: Receptor for TNFRSF11/RANKL/TRANCE/OPGL, essential for
 CC interactions between T-cells and dendritic cells.
 CC -1- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Ubiquitous expression with high levels in
 CC TRABECULAR BONE, THYRUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
 CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
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 DR EMBL: AF019046; AAB8610.1; -;
 DR EMBL: BC019185; AAH19185.1; -;
 DR HSSP: P25942; ICDP.
 DR MGD: MGI:1314891; Tnftrsf11a.
 DR GO: GO:0007275; P:development; IMP.
 DR GO: GO:0007515; P:lymph gland development; IMP.
 DR GO: GO:0001503; P:ossification; IMP.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: Pf00020; TNFR_c6; 3.
 DR SMART: SM00208; TNFR_4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PSS0050; TNFR_NGFR_2; 1.

KW Receptor, Transmembrane, Glycoprotein, Repeat, Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 625
 FT
 FT DOMAIN 31 214
 FT TRANSMEM 215 234
 FT DOMAIN 235 625
 FT REPEAT 35 69
 FT REPEAT 72 113
 FT REPEAT 115 152
 FT REPEAT 155 195
 FT DISULFID 35 47
 FT DISULFID 48 61
 FT DISULFID 51 69
 FT DISULFID 72 87
 FT DISULFID 93 113
 FT DISULFID 115 128
 FT DISULFID 134 152
 FT CARBOHYD 106 106
 FT CARBOHYD 175 175
 FT CONFLICT 494 494
 SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511DBE CRC64;
 Query Match 25.0%; Score 283; DB 1; Length 625;
 Best Local Similarity 32.6%; Pred. No. 5e-17;
 Matches 60; Conservative 25; Mismatches 85; Indels 14; Gaps 4;
 QY 4 QAVPPVASENGQTRDQKEKEYEPQHRICGRCRPGTVASAKCSIRITVCAITCENSNE 63
 Db 30 QVTPPCQD-----RHVEHLGR-CGSRCEGKLSKCTPTSTSVCLPCPDEYLD 79
 QY 64 HWNYLTICQLCRDPDPMWGEETIAPCTSKKTKGRCQCPGMCAMALDCTHCLSDCP 123
 Db 80 TWMEDKCLHAKYCDKALVAVDPGNHTAPRRACIAGH--WNSDCECCRRNTTCAP 136
 QY 124 GTEAEIKDEYKGNHNCVPCAGHPONTSSPSARCQPHTRCENGLVEAAGTAQSDTTC 183
 Db 137 GFGAHPPLQNK-DVTCPTCLGFSDFVSFSTJCKPMTNCTLLGKLEAHQGTESDVVC 195
 QY 184 KNPL 187
 Db 196 SSSM 199
 RESULT 7
 TNRS_HUMAN STANDARD; PRT; 277 AA.
 ID P25942; O9BYU0;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 5 precursor
 DE (CD40L receptor) (B-cell surface antigen CD40) (CDw40) (Bp50).
 GN TNFRSF5 OR CD40.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM I).
 RX MEDLINE=89356608; PubMed=2475341;
 RA Stamenkovic I., Clark E.A., Seed B.;
 RT "A B-lymphocyte activation molecule related to the nerve growth
 RT factor receptor and induced by cytokines in carcinomas.";
 RL EMBO J. 8:1403-1410 (1989).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM I).
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.B., Bridgman A.M., Brown A.J.,
 RA Buck D., Buttrill W.D., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Ciamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslatho M.H., Leverisa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McCormachie L.J., McIlroy K., Murray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA Rice C.M., Ross M.T., Scott C.E., Senta H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sultson J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.,
RA "The DNA sequence and comparative analysis of human chromosome 20.",
RA Nature 414:865-871(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM II).
RX MEDLINE=2111710; PubMed=1172023;
RA "Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.,
RT "Regulation of CD40 function by its isoforms generated through
RT alternative splicing.",
RT Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM I).
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Hootch S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Igoellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.",
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95184010; PubMed=7533327;
RA Cheng G., Cleary A.K., Ye Z.S., Hong D.I., Lederman S., Baltimore D.,
RT "Involvement of CRAF, a relative of TRAF, in CD40 signaling.",
RT Science 267:1494-1498(1995).
RN [6]
RP INTERACTION WITH TRAF3.
RX MEDLINE=95129692; PubMed=7530216;
RA Sato T., Irie S., Reed J.C.,
RT "A novel member of the TRAF family of putative signal transducing
RT proteins binds to the cytosolic domain of CD40.",
RT FEBS Lett. 358:113-118(1995).
RN [7]
RP INTERACTION WITH TRAF1, TRAF2, TRAF3 AND TRAF5.
RX MEDLINE=98384149; PubMed=9718306;
RA Pullen S.S., Miller H.G., Everdeen D.S., Dang T.T., Crute J.J.,
RA Kehry M.R.,
RT "CD40-tumor necrosis factor receptor-associated factor (TRAF)
RT interactions: regulation of CD40 signaling through multiple TRAF

RT binding sites and TRAF hetero-oligomerization.",
RL Biochemistry 37:11836-11845(1998).
RN [8]
RP INTERACTION WITH TRAF5.
RX MEDLINE=98172745; PubMed=9511754;
RA Mitsuhashi S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
RA Otsuka M., Yamamoto T., Inoue J.-I.,
RT "Cloning and characterization of a cDNA encoding the human homolog of
RT tumor necrosis factor receptor-associated factor 5 (TRAF5).",
RL Gene 207:135-140(1998).
RN [9]
RP INTERACTION WITH TRAF6.
RX MEDLINE=98095703; PubMed=9432981;
RA Kashiwada M., Shirakata Y., Inoue J.-I., Nakano H., Okazaki K.,
RA Okamura K., Yamamoto T., Nagao H., Takemori T.,
RT "Tumor necrosis factor receptor-associated factor 6 (TRAF6) stimulates
RT extracellular signal-regulated kinase (ERK) activity in CD40
RT signaling along a ras-independent pathway.",
RL J. Exp. Med. 187:237-244(1998).
RN [10]
RP 3D-STRUCTURE MODELING OF 24-144.
RX MEDLINE=97189482; PubMed=9037712;
RA Bajorek J., Arnulfo A.,
RT "Construction and analysis of a detailed three-dimensional model of
RT the ligand binding domain of the human B cell receptor CD40.",
RL Proteins 27:59-70(1997).
RN [11]
RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.
RX MEDLINE=9826353; PubMed=960517,
RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RA Zheng Z., Naismith J.H., Thomas D.,
RT "The role of polar interactions in the molecular recognition of CD40L
RT with its receptor CD40.",
RL Protein Sci. 7:1124-1135(1998).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF 247-266 IN COMPLEX WITH
RP TRAF3.
RX MEDLINE=20442386; PubMed=10984535;
RA Ni C.Z., Welch K., Leo E., Chou C.K., Wu H., Reed J.C., Ely K.R.,
RT "Molecular basis for CD40 signaling mediated by TRAF3.",
RL Proc. Natl. Acad. Sci. U.S.A. 97:10395-10399(2000).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 178-195 IN COMPLEX WITH
RP TRAF3.
RX MEDLINE=22000222; PubMed=12005438;
RA Li C., Ni C.Z., Havert M.L., Cabezas E., He J., Kaiser D., Reed J.C.,
RA Satterthwaite A.C., Cheng G., Ely K.R.,
RT "Downstream regulator TRAF3 binds to the CD40 recognition site on
RT TRAF3.",
RL Structure 10:403-411(2002).
RN [14]
RP VARIANT HIGM3 ARG-83.
RX MEDLINE=21532985; PubMed=11675497;
RA Ferrari S., Gillani S., Insalaco A., Al-Chonaim A., Sorensen A.R.,
RA Loubser M., Avanzini M.A., Marconi M., Badiolati R., Ugaizo A.G.,
RA Levy Y., Catalan N., Durandy A., Tbakhi A., Notarangelo L.D.,
RA Plebani A.,
RT "Mutations of CD40 gene cause an autosomal recessive form of
RT immunodeficiency with hyper IgM.",
RT Proc. Natl. Acad. Sci. U.S.A. 98:12614-12619(2001).
RN [15]
RP FUNCTION: Receptor for TNFSF5/CD40L.
CC - FUNCTION: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC - SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC - SUBCELLULAR LOCATION: Type I membrane protein (isoform I);
CC secreted (isoform II).
CC - ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=I;
CC IsoId=P25942-1; Sequence=Displayed;
CC Name=II;
CC IsoId=P25942-2; Sequence=VSP_006472; VSP_006473;
CC - TISSUE SPECIFICITY: B-cells and in primary carcinomas.
CC - DISEASE: Defects in TNFRSF5 are the cause of hyper-IgM


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CC immunodeficiency type 3 (HIGM3) [MIM:606843]. HIGM3 is an
CC autosomal recessive disorder which includes an inability of B
CC cells to undergo isotype switching, one of the final
CC differentiation steps in the humoral immune system, an inability
CC to mount an antibody-specific immune response, and a lack of
CC germinal center formation.
CC
CC -! SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -! DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X60592; CAA43045.1; -
CC DR EMBL; AL035662; CAC17670.1; -
CC DR EMBL; AJ300189; CAC29424.1; -
CC DR EMBL; BC012419; AAH12419.1; -
CC DR PIR; S04460; A60771.
CC DR PDB; 1CDF; 01-APR-97.
CC DR PDB; 1FIL; 18-OCT-00.
CC DR PDB; 1LOA; 08-FEB-00.
CC DR PDB; 1CZ2; 26-SEP-01.
CC
CC Query Match 24.5%; Score 278; DB 1; Length 277;
CC Best Local Similarity 35.0%; Pred. No. 6,1e-17;
CC Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;
CC
CC QY 7 PPVASENQTGRDQKEXYEPQHRICSGRPPTVYSAKSGRIRDTVCATGANSYNHWN 66
CC DB 22 PPTA-----CR--EKQYLINSQ--CCLCQPGKVLVDTEFTFTECTLPGGESEFLDTWN 72
CC QY 67 YLTICQLCRPCDPVMEGBELAPCTSKKTKQCRCQPGFCAAMALECHHELSDCPGTE 126
CC DB 73 RETHCHQHKYCDPMLGLRVQCKGISEDTTCTCEBGMHCTSEA--CSCVLSHSCSPGFG 130
CC QY 127 AELKDEVGKNNHCVPCKAGHFONTSSPASCOPHTRCENOGVEAPAGTASPTTC 183
CC DB 131 VK-QIATGVSDTICEPCPVGFSSVSAFCKCHWTCTCKDLVVOAGINKIDVVC 186
CC
CC RESULT 8
CC TR11 HUMAN STANDARD; PRT; 616 AA.
CC AC 09Y606;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Tumor necrosis factor receptor superfamily member 11A precursor
CC DE (Receptor activator of NF-KB) (Osteoclast differentiation factor
CC DE receptor) (ODFR).
CC GN TNFRSF11A OR RANK.
CC OS Homo sapiens (human).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN 1;
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Dendritic cell;
CC RA MEDLINE=98032977; PubMed=9367155;
CC RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
CC RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
CC RA Galibert L.;
CC RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
CC RT and dendritic-cell function.";
CC RL Nature 390:175-179 (1997).
CC RN 12;
CC RP FUNCTION.
CC RX MEDLINE=99097247; PubMed=9878548;

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RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RA "RANK is the essential signaling receptor for osteoclast
RA differentiation factor in osteoclastogenesis.";
RA Biochem. Biophys. Res. Commun. 253:395-400(1998).
RA
RA [3]
RA INTERACTION WITH TRAF1, TRAF2, TRAF3, TRAF5 AND TRAF6.
RA MEDLINE=98447691; PubMed=9774460;
RA Wong B.R., Jostien R., Lee S.Y., Vologodskaya M., Steinman R.M.,
RA Choi Y.;
RA "The TRAF family of signal transducers mediates NF-kappaB activation
RA by the TRANCE receptor.";
RA J. Biol. Chem. 273:28355-28359(1998).
RA
RA [4]
RA VARIANT FEO LEU-LEU-CYS-ALA-LEU-LEU-21 INS. VARIANT PDB2
RA ALA-LEU-LEU-LEU-LEU-CYS-ALA-LEU-LEU-21 INS. AND VARIANT VAL-192.
RA MEDLINE=20082806; PubMed=10615125;
RA Hughes A.E., Ralston S.H., Marken J., Bell C., Macpherson H.,
RA Wallace R.G.H., van Hal W., Whyte M.P., Nakatsuka K., Hoy L.,
RA Anderson D.M.;
RA "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
RA familial expansile osteolysis.";
RA Nat. Genet. 24:45-48(2000).
RA
RA -! FUNCTION: Receptor for TNFRSF11/RANKL/TRANCE/OPGL, essential for
RA RANKL-mediated osteoclastogenesis. Involved in the regulation of
RA interactions between T-cells and dendritic cells.
RA -! SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
RA -! TISSUE SPECIFICITY: Ubiquitous expression with high levels in
RA skeletal muscle, thymus, liver, colon, small intestine and adrenal
RA gland.
RA -! DISEASE: Defects in TNFRSF11A are the cause of familial expansile
RA osteolysis (FEO) [MIM:174810]. FEO is a rare autosomal dominant
RA bone disorder characterized by focal areas of increased bone
RA remodelling. The osteolytic lesions develop usually in the long
RA bones during early adulthood. FEO is often associated with early
RA onset deafness and loss of dentition.
RA -! DISEASE: Defects in TNFRSF11A are a cause of Paget disease of bone
RA 2 (PDB2) [MIM:602080]; also known as familial Paget disease of
RA bone. PDB2 is a bone remodelling disorder with clinical
RA similarities to FEO. Unlike FEO, however, affected individuals
RA have involvement of the axial skeleton with lesions in the spine,
RA pelvis and skull.
RA
RA -! SIMILARITY: Contains 4 TNFR-Cys repeats.
RA
RA This SWISS-PROT entry is copyright. It is produced through a collaboration
RA between the Swiss Institute of Bioinformatics and the EMBL outstation -
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RA
RA EMBL; AF018253; AAB86809.1; -
RA HSSP; P25942; 1CDF.
RA DR Genew; HGNC:11908; TNFRSF11A.
RA DR MIM; 603499; -
RA DR MIM; 174810; -
RA DR MIM; 602080; -
RA DR GO; GO:0004872; F:receptor activity; TAS.
RA DR GO; GO:0007267; P:cell-cell signaling; TAS.
RA DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
RA DR GO; GO:0007165; P:signal transduction; TAS.
RA DR InterPro; IPR001368; TNFR_c6.
RA DR Pfam; PF00020; TNFR_c6; 4.
RA DR SMART; SM00208; TNFR_4.
RA DR PROSITE; PS00652; TNFR_NGFR_1; 1.
RA DR PROSITE; PS00500; TNFR_NGFR_2; 1.
RA KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
RA Disease mutation; Deafness.
RA FT SIGNAL 1 29
RA FT CHAIN 30 616
RA
RA POTENTIAL.
RA TUMOR NECROSIS FACTOR RECEPTOR
RA SUPERFAMILY MEMBER 11A.

```

FT	DOMAIN	30	212	EXTACELLULAR (POTENTIAL) .
FT	TRANSMEM	213	233	POTENTIAL.
FT	DOMAIN	234	616	CYTOPLASMIC (POTENTIAL) .
FT	REPEAT	34	68	TNFR-CYS 1.
FT	REPEAT	71	112	TNFR-CYS 2.
FT	REPEAT	114	151	TNFR-CYS 3.
FT	REPEAT	154	194	TNFR-CYS 4.
FT	DISULFID	34	46	BY SIMILARITY.
FT	DISULFID	47	60	BY SIMILARITY.
FT	DISULFID	50	68	BY SIMILARITY.
FT	DISULFID	71	86	BY SIMILARITY.
FT	DISULFID	92	112	BY SIMILARITY.
FT	DISULFID	114	127	BY SIMILARITY.
FT	DISULFID	133	151	BY SIMILARITY.
FT	CARBOHYD	105	105	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	174	174	N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	VARIANT	21	21	L -> LALLICALL (in PDB2).
FT	VARIANT	21	21	/FTID=VAR_011516.
FT	VARIANT	21	21	L -> LILICALL (in FEO).
FT	VARIANT	192	192	/FTID=VAR_011517.
FT	VARIANT	192	192	A -> V.
FT	VARIANT	192	192	/FTID=VAR_011518.
SO	SEQUENCE	616 AA;	66033 MM;	ESDDE9A7A08196F81 CRC64;
Query Match		24.4%;	Score 277;	DB 1;
Best Local Similarity		31.7%;	Pred. No. 1.6e-16;	Length 616;
Matches	60;	Conservative	28;	Mismatches 87;
				Indels 14;
				Gaps 4
QY	4	QAVPPVASENQCIRBQKEVEYEPQRRICCSRCPPGTIVYSAKCSRTRDYCATCAENS	YNE 63	
DB	29	QIAPPCPSE-----KHVEHLGR-CCKCEPKKMSKKTTSDSVCLPCGPDYILD	78	
QY	64	HMNYLITTCQLCRPCDPVNGLEELIAPCTSKRTQCRQPMFCAMALECTHCELLISDCP	123	
DB	79	SMNEEDCKCLLHKVCGTGLKALVAVVAGNSTTPRCACCTAGYH--WSQCECCRRNTECAP	135	
QY	124	GTEAEFLKBEVGKGNHHCYPCYKAGHGQUNSSPPARCOPIHRCENQGLVEAPGTAQSDPTTC	183	
DB	136	GLGAGHPVLQLNK-DIVCKPCLAGYFSDAFSSDCKRPMWNTCTFLGRVHHGTETSDAVC	194	
QY	184	KNPLEPLPP	192	
DB	195	SSSUPARKP	203	
RESULT 9				
TNRS	BOVIN	STANDARD;	PRT;	269 AA.
ID	TNRS_BOVIN	STANDARD;	PRT;	269 AA.
AC	028203;			
DI	01-NOV-1997 (rel. 35, Created)			
DI	01-NOV-1997 (rel. 35, Last sequence update)			
DI	10-OCT-2003 (rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 5 precursor			
DE	(CD40L receptor) (B-cell surface antigen CD40) (Fragment).			
GN	TNFRSF5 OR CD40.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97281252; PubMed=9135560;			
RA	Hirano A., Brown W.C., Estes D.M.;			
RT	"Cloning, expression and biological function of the bovine CD40			
RT	homologue: role in B-lymphocyte growth and differentiation in			
RT	cattle.";			
RL	Immunology 90:294-300(1997).			
CC	-I- FUNCTION: Receptor for TNFRSF5/CD40L.			
CC	-I- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By			
CC	similarity).			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-I- SIMILARITY: Contains 4 TNFR-Cys repeats.			

Query Match	Best Local Similarity	Matches	Score	DB 1	Length	DB 2	Score	DB 3	Length	DB 4	Score	DB 5	Length	DB 6	Score	DB 7	Length	DB 8	Score	DB 9	Length	DB 10	Score	DB 11	Length	DB 12	Score	DB 13	Length	DB 14	Score	DB 15	Length	DB 16	Score	DB 17	Length	DB 18	Score	DB 19	Length	DB 20	Score	DB 21	Length	DB 22	Score	DB 23	Length	DB 24	Score	DB 25	Length	DB 26	Score	DB 27	Length	DB 28	Score	DB 29	Length	DB 30	Score	DB 31	Length	DB 32	Score	DB 33	Length	DB 34	Score	DB 35	Length	DB 36	Score	DB 37	Length	DB 38	Score	DB 39	Length	DB 40	Score	DB 41	Length	DB 42	Score	DB 43	Length	DB 44	Score	DB 45	Length	DB 46	Score	DB 47	Length	DB 48	Score	DB 49	Length	DB 50	Score	DB 51	Length	DB 52	Score	DB 53	Length	DB 54	Score	DB 55	Length	DB 56	Score	DB 57	Length	DB 58	Score	DB 59	Length	DB 60	Score	DB 61	Length	DB 62	Score	DB 63	Length	DB 64	Score	DB 65	Length	DB 66	Score	DB 67	Length	DB 68	Score	DB 69	Length	DB 70	Score	DB 71	Length	DB 72	Score	DB 73	Length	DB 74	Score	DB 75	Length	DB 76	Score	DB 77	Length	DB 78	Score	DB 79	Length	DB 80	Score	DB 81	Length	DB 82	Score	DB 83	Length	DB 84	Score	DB 85	Length	DB 86	Score	DB 87	Length	DB 88	Score	DB 89	Length	DB 90	Score	DB 91	Length	DB 92	Score	DB 93	Length	DB 94	Score	DB 95	Length	DB 96	Score	DB 97	Length	DB 98	Score	DB 99	Length	DB 100	Score	DB 101	Length	DB 102	Score	DB 103	Length	DB 104	Score	DB 105	Length	DB 106	Score	DB 107	Length	DB 108	Score	DB 109	Length	DB 110	Score	DB 111	Length	DB 112	Score	DB 113	Length	DB 114	Score	DB 115	Length	DB 116	Score	DB 117	Length	DB 118	Score	DB 119	Length	DB 120	Score	DB 121	Length	DB 122	Score	DB 123	Length	DB 124	Score	DB 125	Length	DB 126	Score	DB 127	Length	DB 128	Score	DB 129	Length	DB 130	Score	DB 131	Length	DB 132	Score	DB 133	Length	DB 134	Score	DB 135	Length	DB 136	Score	DB 137	Length	DB 138	Score	DB 139	Length	DB 140	Score	DB 141	Length	DB 142	Score	DB 143	Length	DB 144	Score	DB 145	Length	DB 146	Score	DB 147	Length	DB 148	Score	DB 149	Length	DB 150	Score	DB 151	Length	DB 152	Score	DB 153	Length	DB 154	Score	DB 155	Length	DB 156	Score	DB 157	Length	DB 158	Score	DB 159	Length	DB 160	Score	DB 161	Length	DB 162	Score	DB 163	Length	DB 164	Score	DB 165	Length	DB 166	Score	DB 167	Length	DB 168	Score	DB 169	Length	DB 170	Score	DB 171	Length	DB 172	Score	DB 173	Length	DB 174	Score	DB 175	Length	DB 176	Score	DB 177	Length	DB 178	Score	DB 179	Length	DB 180	Score	DB 181	Length	DB 182	Score	DB 183	Length	DB 184	Score	DB 185	Length	DB 186	Score	DB 187	Length	DB 188	Score	DB 189	Length	DB 190	Score	DB 191	Length	DB 192	Score	DB 193	Length	DB 194	Score	DB 195	Length	DB 196	Score	DB 197	Length	DB 198	Score	DB 199	Length	DB 200	Score	DB 201	Length	DB 202	Score	DB 203	Length	DB 204	Score	DB 205	Length	DB 206	Score	DB 207	Length	DB 208	Score	DB 209	Length	DB 210	Score	DB 211	Length	DB 212	Score	DB 213	Length	DB 214	Score	DB 215	Length	DB 216	Score	DB 217	Length	DB 218	Score	DB 219	Length	DB 220	Score	DB 221	Length	DB 222	Score	DB 223	Length	DB 224	Score	DB 225	Length	DB 226	Score	DB 227	Length	DB 228	Score	DB 229	Length	DB 230	Score	DB 231	Length	DB 232	Score	DB 233	Length	DB 234	Score	DB 235	Length	DB 236	Score	DB 237	Length	DB 238	Score	DB 239	Length	DB 240	Score	DB 241	Length	DB 242	Score	DB 243	Length	DB 244	Score	DB 245	Length	DB 246	Score	DB 247	Length	DB 248	Score	DB 249	Length	DB 250	Score	DB 251	Length	DB 252	Score	DB 253	Length	DB 254	Score	DB 255	Length	DB 256	Score	DB 257	Length	DB 258	Score	DB 259	Length	DB 260	Score	DB
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ID	TI1B_MOUSE	STANDARD:	PERT:	401 AA.
AC	008712;	070202;		
DT	28-FEB-2003	(Rel. 41, Created)		
DT	28-FEB-2003	(Rel. 41, last sequence update)		
DT	28-FEB-2003	(Rel. 41, last annotation update)		
DE	Tumor necrosis factor receptor superfamily member 11B precursor			
DE	(osteoprotegerin) (osteoclastogenesis inhibitory factor).			
GN	TNFRSF11B OR OPG OR OCIF.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxId=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c; TISSUE=Kidney;			
RA	MEDLINE=97262071; PubMed=9108485;			
RA	Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,			
RA	Deuse M., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,			
RA	Lacey M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,			
RA	Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Patlison W.,			
RA	Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,			
RA	Suggs S., Boyle W.J.,			
RT	"Osteoprotegerin: a novel secreted protein involved in the regulation			
RT	of bone density."			
RL	Cell 89:309-319(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288			
RC	AND ARG-296			
RA	STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;			
RA	MEDLINE=99382527; PubMed=9714933;			
RA	Minano A., Mitrakmi A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,			
RA	Higashio K.;			
RT	"Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)			
RT	gene and its expression in embryogenesis";			
RL	Gene 215:339-343(1998).			
RN	[3]			
RP	FUNCTION.			
RA	MEDLINE=21060987; PubMed=10952716;			
RA	Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,			
RA	Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,			
RA	Simonet W.S.;			
RT	"Osteoprotegerin reverses osteoporosis by inhibiting endosteal			
RT	osteoclasts and prevents vascular calcification by blocking a process			
RT	resembling osteoclastogenesis."			
RL	J. Exp. Med. 192:463-474(2000).			
CC	-1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes			
CC	its function in osteoclastogenesis. Inhibits the activation of			
CC	osteoclasts and promotes osteoclast apoptosis in vitro. Bone			
CC	homeostasis seems to depend on the local RANKL/OPG ratio. May also			
CC	play a role in preventing arterial calcification. May act as decoy			
CC	receptor for TRAIL and protect against apoptosis. TRAIL binding			
CC	blocks the inhibition of osteoclastogenesis.			
CC	-1- SUBUNIT: Homodimer.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,			
CC	intestines and calvaria. Highly expressed in decidua and placenta,			
CC	and in embryo.			
CC	-1- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,			
CC	whereas expression decreases at day 11 and increases from day 15			
CC	to 17. On day 15 found in developing bone primordia,			
CC	brachiocephalic artery and ductus arteriosus, left main bronchus,			
CC	abdominal aorta and midgut.			
CC	-1- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by			
CC	1,25-dihydroxyvitamin D3 and parathyroid hormone.			
CC	-1- SIMILARITY: Contains 4 TNF-Cys repeats.			
CC	-1- SIMILARITY: Contains 2 death domains.			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	its European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			

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CC	entities requires a license agreement (See http://www.isb.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; U9431; AAB53708.1; -
DR	EMBL; AB013898; BAA28269.1; -
DR	EMBL; AB013903; BAA33388.1; -
DR	EMBL; AB013899; BAA33388.1; JOINED.
DR	EMBL; AB013900; BAA33388.1; JOINED.
DR	EMBL; AB013901; BAA33388.1; JOINED.
DR	EMBL; AB013902; BAA33388.1; JOINED.
DR	HSSP; P25942; ICDF.
DR	MGP; MGI:109587; Tnfrcflb.
DR	GO; GO:0005578; C:extracellular matrix; IDA.
DR	InterPro; IPR00488; Death.
DR	InterPro; IPR01368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 3.
DR	SMART; SM00208; TNFR; 4.
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.
DR	PROSITE; PS00500; TNFR_NGFR_2; 2.
KW	Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT	SIGNAL 1 21
FT	CHAIN 22 401
FT	REPEAT 24 62
FT	REPEAT 65 105
FT	REPEAT 107 142
FT	REPEAT 145 185
FT	DOMAIN 198 269
FT	DOMAIN 283 365
FT	SITE 400 400
FT	DISULFID 41 54
FT	DISULFID 44 62
FT	DISULFID 65 80
FT	DISULFID 83 97
FT	DISULFID 87 105
FT	DISULFID 107 118
FT	DISULFID 124 142
FT	DISULFID 145 160
FT	DISULFID 166 185
FT	CARBOHYD 98 98
FT	CARBOHYD 165 165
FT	CARBOHYD 178 178
FT	CARBOHYD 289 289
FT	VARIANT 138 138
FT	VARIANT 161 161
FT	VARIANT 165 165
FT	VARIANT 288 288
FT	VARIANT 296 296
FT	SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;
QY	Query Match 21.4%; Score 242.5; DB 1; Length 401;
QY	Best Local Similarity 29.6%; Pred. No. 9.4e-14;
QY	Matches 50; Conservative 25; Mismatches 83; Indels 11; Gaps 5
Db	23 YEPQ--HRIICSRCPGTYVSAKCSIRIDYCATCAENSYNENHMYLTICQLCRP-CDP 79
Db	30 HYDEPETHQLODCKAPGYTLKQHCIVRRKTLICVPCPDHSDYSDMHTSDCEYVCSVCKE 89
QY	VMGLEIAPCTSKRKTQCRCQRCQPMFCMAALAEETHHEILSDCPRTGEALDKQEVGSGNNH 139
Db	90 LOSVKO--ECNRTTHNVCECEGRY-----LEIEFLIKHRCSPGS-GVVAQATPERNTV 141
QY	140 CVYCKAGHQNTPSPSARCOPIHRCENOGIJEVAAPTAQSDTTCNNPLE 188
Db	142 CKKCPDGFSPGSETSKAPCLKHNCTFGILLIQQKNAHTDNCVCSNRE 190

RESULT 12
 T11B_HUMAN
 ID T11B_HUMAN STANDARD; FRT; 401 AA.
 AC 000300; 060236; Q9UHP4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11B precursor
 DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
 GN TNFRSF11B OR OPG OR OCIF.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luthy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density.";
 RL Cell 89:309-319(1997).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung cancer;
 RX MEDLINE=9815103; PubMed=9492069;
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
 RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
 RA Tsuda E., Morinaga T., Higashio K.;
 RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and
 RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
 RT osteoclastogenesis in vitro.";
 RL Endocrinology 139:1329-1337(1998).
 [3]
 RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
 RC TISSUE=Placenta;
 RX MEDLINE=9831569; PubMed=9688283;
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
 RT "Cloning and characterization of the gene encoding human
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
 RL Eur. J. Biochem. 254:685-691(1998).
 [4]
 RP SEQUENCE FROM N.A., AND VARIANT ASN-3.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schlier G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang U., Hsieh L.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.D., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalón D.K., Muray D.M., Sodegren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Truchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gittman J.E., Jones S.J.M., Maitra M.A.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maitra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [5]

RP SEQUENCE OF 22-36 AND 378-401.
 RX MEDLINE=98238645; PubMed=9571159;
 RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
 RA Morinaga T., Tsuda E., Higashio K.;
 RT "Characterization of monomeric and homodimeric forms of
 RT osteoclastogenesis inhibitory factor.";
 RL Biochem. Biophys. Res. Commun. 245:382-387(1998).
 [6]
 RP SEQUENCE OF 22-393 FROM N.A.
 RC TISSUE=Placenta;
 RT "Cloning and expression of osteoprotegerin from Homo sapiens.";
 RL Acta Biochim. Biophys. Sin. 31:680-684(1999).
 [7]
 RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
 RX MEDLINE=97312536; PubMed=9168977;
 RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
 RA Morinaga T., Higashio K.;
 RT "Isolation of a novel cytokine from human fibroblasts that
 RT specifically inhibits osteoclastogenesis.";
 RL Biochem. Biophys. Res. Commun. 234:137-142(1997).
 [8]
 RP TRAIL BINDING.
 RX MEDLINE=98269100; PubMed=9603945;
 RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
 RA Dahl E., Appelbaum E.R., Richman C., DiPrinzio R., Dadds R.A.,
 RA James I.E., Rosenberg M., Lee J.C., Young P.R.;
 RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
 RL J. Biol. Chem. 273:14363-14367(1998).
 [9]
 RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
 RX MEDLINE=98148058; PubMed=9478964;
 RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
 RA Morinaga T., Higashio K.;
 RT "Characterization of structural domains of human osteoclastogenesis
 RT inhibitory factor.";
 RL J. Biol. Chem. 273:5117-5123(1998).
 [10]
 RP REVIEW.
 RX MEDLINE=21395914; PubMed=11505389;
 RA Hofbauer L.C., Neuberger A., Heutelder A.E.;
 RT "Receptor activator of nuclear factor-kappaB ligand and
 RT osteoprotegerin: potential implications for the pathogenesis and
 RT treatment of malignant bone diseases.";
 RL Cancer 92:460-470(2001).
 CC -1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
 CC its function in osteoclastogenesis. Inhibits the activation of
 CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
 CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
 CC play a role in preventing arterial calcification.
 CC receptor for TRAIL and protect against apoptosis. TRAIL binding
 CC blocks the inhibition of osteoclastogenesis.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
 CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
 CC lymph node, trachea, adrenal gland, testis, and bone marrow.
 CC detected at very low levels in brain, placenta and skeletal
 CC muscle. Highly expressed in fetal kidney, liver and lung.
 CC -1- INDUCTION: Upregulated by increasing calcium-concentration in the
 CC medium and estrogens. Downregulated by glucocorticoids.
 CC -1- PTM: N-glycosylated. Contains static acid residues.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 2 death domains.
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CC -----
DR EMBL: U94330; AAB53707.1; -.
DR EMBL: AB002146; BAA25910.1; -.
DR EMBL: AB008822; BAA32076.1; -.
DR EMBL: AB008821; BAA32076.1; JOINED.
DR EMBL: BC030155; AAB30155.1; -.
DR EMBL: AF134187; AAF20168.1; -.
DR HSSP; P25942; ICDF.
DR Genew; HGNC:11909; TNFRSF11B.
DR MIM; 602643; -.
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0005125; F:cytokine activity; TAS.
DR GO; GO:0004872; P:receptor activity; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR GO; GO:0001501; P:skeletal development; TAS.
DR InterPro; IPR00488; Death.
DR InterPro; IPR01368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 401
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT REPEAT 198 269
FT DOMAIN 270 365
FT SITE 400 400
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 105 118
FT DISULFID 124 142
FT DISULFID 145 160
FT DISULFID 166 185
FT CARBOHYD 98 98
FT CARBOHYD 152 152
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
FT VARIANT 3 3
FT MUTAGEN 400 400
FT MUTAGEN 401 401
FT CONFLICT 263 263
SQ SEQUENCE 401 AA; 46040 MW; EDF448B67D86C71E CRC64;

Query Match 21.1%; Score 239.5; DB 1; Length 401;
Best Local Similarity 30.9%; Pred. No. 1.7e-13;
Matches 51; Conservative 21; Mismatches 84; Indels 9; Gaps 4;

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TT1B_RAT
ID TT1B_RAT STANDARD; PRT; 401 AA.
AC 008727;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (osteoprotegerin).
GN TNFRSF11B OR ORF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic intestine;
RX MEDLINE=97262071; Pubmed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Linethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy B., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.,
RT "Osteoprotegerin: a novel secreted protein involved in the regulation
RT of bone density."
RL Cell 89:309-319(1997).
CC -1- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC seems to depend on the local RANKL/OPG ratio. May also play a role
CC in preventing arterial calcification. May act as decoy receptor
CC for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC inhibition of osteoclastogenesis (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- INDUCTION: Upregulated by osteopontin.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -1- SIMILARITY: Contains 2 death domains.
CC -----
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CC -----
DR EMBL: U94330; AAB53707.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR00488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; FALSE_NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT REPEAT 198 269
FT DOMAIN 270 365
FT SITE 400 400
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105

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FT DISULFID 107 118 BY SIMILARITY.
 FT DISULFID 124 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT DISULFID 166 185 BY SIMILARITY.
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 401 AA; FE6A31FD4E573A CRC64;
 Query Match 20.8%; Score 235.5; DB 1; Length 401;
 Best Local Similarity 29.6%; Pred. No. 3.7e-13;
 Matches 50; Conservative 24; Mismatches 84; Indels 11; Gaps 5;
 QY 23 YYPEPQ--HRICCSRPCTGYSAKSRIRDTVCATCAENSYNEHNNYLTICQLCRP--CDP 79
 DB 30 HYDEPTGRLLCDCRACPGTYLKQCTVARKTLVCPDPYSTDSWHTSDECVYCSPVCKE 89
 QY 80 VMGLEELIAPCTSKRKTQCRCPGMCAMALECHCELLSDCPGTETELKDEYKGNH 139
 DB 90 LQTVKQ--ECNRTNRRVCEEGRY----LELEPCLKHSRCPQL--GVLDAGTPERTV 141
 QY 140 CVPCKAGHPONTSSPSARCOPHTRCENQGLVEAPGTAQSDPTCKNPLE 188
 DB 142 CKRCPDGFFSGSTSSKAPCRKHTNCSSILGLLQKGNATHNVCSGNRE 190
 RESULT 14
 ID TR14 HUMAN STANDARD; PRT; 283 AA.
 AC Q92956; Q8WXR1; Q96J31; Q9UM65;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 14 precursor
 DE (Herpesvirus entry mediator A) (Tumor necrosis factor receptor-like 2)
 DE (TR2).
 GN TNFRSF14 OR HVEM OR HVMA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervical adenocarcinoma;
 RX MEDLINE=97053782; PubMed=898196;
 RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
 RT "Herpes simplex virus-1 entry into cells mediated by a novel member of
 the TNF/NGF receptor family.";
 RL Cell 87:427-436(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97306336; PubMed=9162061;
 RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
 RA Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
 RA Porter T.G., Tumbah A., Young P.R.;
 RT "A newly identified member of the tumor necrosis factor receptor
 superfamily with a wide tissue distribution and involvement in
 lymphocyte activation.";
 RL J. Biol. Chem. 272:14272-14276(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Zhang W., Man T., Cao X.;
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.
 RX MEDLINE=21629477; PubMed=11756979;
 RA Struyf F., Posavac C.M., Keyaerts E., Van Raest M., Corey L.,
 RA Spear P.G.;
 RT "Search for polymorphisms in the genes for herpesvirus entry mediator,
 Nectin-1, and Nectin-2 in immune seronegative individuals.";
 RL J. Infect. Dis. 185:36-44(2002).
 RN [5]

RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shermen C.W., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Uedon T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguelfano N.A., Peters G.J., Adrison R.D., Mollahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP INTERACTION WITH TRAF2 AND TRAF5.
 RX MEDLINE=97298041; PubMed=9153189;
 RA Hsu H., Solovayev I., Colombero A., Elliott R., Kelley M., Boyle W.J.;
 RT "ATRA, a novel tumor necrosis factor receptor family member, signals
 through TRAF2 and TRAF5.";
 RL J. Biol. Chem. 272:13471-13474(1997).
 RN [7]
 RP INTERACTION WITH TRAF3 AND TRAF5.
 RX MEDLINE=97306297; PubMed=9162022;
 RA Marsters S.A., Ayres T.M., Skubatch M., Gray C.L., Rothe M.,
 RA Ashkenazi A.;
 RT "Herpesvirus entry mediator, a member of the tumor necrosis factor
 receptor (TNFR) family, interacts with members of the TNFR-associated
 factor family and activates the transcription factors NF-kappaB and
 AP-1.";
 RL J. Biol. Chem. 272:14029-14032(1997).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
 RX MEDLINE=21403268; PubMed=11511370;
 RA Carli A., Willis S.H., Whitbeck J.C., Krummenacher C., Cohen G.H.,
 RA Eisenberg R.J., Wiley D.C.;
 RT "Herpes simplex virus glycoprotein D bound to the human receptor
 Hvea.";
 RL Mol. Cell 8:169-179(2001).
 CC -I- FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric
 TNFSF14/lymphotoxin-alpha. Involved in lymphocyte activation. Plays
 CC an important role in HSV pathogenesis because it enhanced the
 CC entry of several wildtype HSV strains of both serotypes into CHO
 CC cells, and mediated HSV entry into activated human T cells.
 CC -I- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
 CC -I- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
 CC IN LUNG, SPLEEN, AND THYMUS.
 CC -I- SIMILARITY: Contains 3 TNFR-Cys repeats.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC -----
 CC EMBL, U70321; AAB58354.1; -
 CC EMBL, U81232; AAD0505.1; -
 CC EMBL, AF153978; AAF75588.1; -
 CC EMBL, AF378877; AAL47717.1; -
 CC EMBL, AF378878; AAL47718.1; -
 CC EMBL, BC002794; AAH02794.1; -

CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; AF068868; AAC34583.1; -
DR EMBL; AL096801; CAB75692.1; -
DR EMBL; BC017730; AAH17730.1; -
DR EMBL; BC010241; AAH10241.1; ALT_INIT.
DR HSSP; O14763; IDOG.
DR Genew; HGNC:13469; TNFRSF21.
DR MIM; 605732; -
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS50017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
DR Receptor; Apoptosis; Transmembrane; Repeat; signal.
FT SIGNAL 1 41
FT CHAIN 42 655
FT FT 42 655
FT DOMAIN 42 655
FT TRANSMEM 350 370
FT DOMAIN 371 655
FT DOMAIN 415 498
FT REPEAT 50 88
FT REPEAT 90 131
FT REPEAT 133 167
FT REPEAT 170 211
FT DISULFID 67 80
FT DISULFID 70 88
FT DISULFID 91 106
FT DISULFID 109 123
FT DISULFID 113 131
FT DISULFID 133 144
FT DISULFID 150 168
FT DISULFID 171 186
FT DISULFID 192 211
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FT CARBOHYD 141 141
FT CARBOHYD 252 252
FT CARBOHYD 257 257
FT CARBOHYD 278 278
FT CARBOHYD 289 289
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Query Match
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Matches 56; Conservative 23; Mismatches 65; Indels 37; Gaps 8;

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Db 65 LHCDDKCPAGTYVSEHNTSLKVCSSCPGVTFRHENGIEKCHDCQPC-PWMTKEL-P 122
QY 89 CTSKRKTQCRQDGMF-----CAWALBCTHCELLSDCP-----PSTEAEIKDEVGKG 136
Db 123 CAALTDRECTCPFGMFGSNATCAPHTV-----CPVGMGVRKKGTE----- 164
QY 137 NNHCVPCXKXGHQNTSPSARCPHRCENCGIVEAPGTAOSDTTCKNPLEPLPEMSG 196
Db 165 DVRCXQCARGTSDVSSVWCKKAYIDLSQNLVVIKPGTKETDNCVT---LPSFSSS 220
QY 197 T 197
Db 221 T 221

Search completed: August 27, 2004, 21:08:21
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 27, 2004, 21:05:51 ; Search time 32 Seconds

(without alignments)
317,822 Million cell updates/sec

Title: US-09-626-219-1

Perfect score: 1133

Sequence: 1 SQQAVPVYASENQTCDQF.....QSDTTCKNPLELPPEKSGT 197

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/2/1aa/5B COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B COMB.pep:*
5: /cgn2_6/prodata/2/1aa/6CTUS COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	100.0	197	2	US-08-505-606-1
2	1133	100.0	197	4	US-09-000-166-1
3	1133	100.0	197	4	US-09-303-262-1
4	987	87.1	170	4	US-08-828-683A-14
5	981	86.6	170	4	US-09-523-323-57
6	771	68.0	415	3	US-09-006-353A-6
7	771	68.0	415	3	US-09-573-986-6
8	456	40.2	77	3	US-08-866-545-3
9	456	40.2	77	3	US-09-627-775-3
10	305	26.9	227	3	US-08-974-023-48
11	305	26.9	227	3	US-08-795-445A-48
12	305	26.9	227	3	US-08-974-186-48
13	305	26.9	227	3	US-08-974-186-48
14	305	26.9	227	3	US-08-795-446B-48
15	305	26.9	227	4	US-08-706-945B-134
16	305	26.9	227	4	US-08-577-788C-48
17	305	26.9	235	4	US-09-326-394-4
18	305	26.9	235	4	US-09-580-235-2
19	305	26.9	235	4	US-09-580-235-2
20	305	26.9	235	4	US-09-580-235-8
21	305	26.9	235	4	US-09-580-181-2
22	305	26.9	235	4	US-09-580-181-8
23	305	26.9	235	4	US-09-102-530-2
24	305	26.9	235	4	US-09-102-530-8
25	305	26.9	257	4	US-09-579-845-10
26	305	26.9	461	1	US-08-385-229-2
27	305	26.9	461	3	US-09-042-785A-7

28	305	26.9	461	3	US-08-477-347-3	Sequence 3, Appli
29	305	26.9	461	3	US-09-006-353A-4	Sequence 4, Appli
30	305	26.9	461	3	US-08-476-862-2	Sequence 2, Appli
31	305	26.9	461	4	US-09-573-986-4	Sequence 4, Appli
32	305	26.9	461	4	US-08-406-824A-2	Sequence 2, Appli
33	305	26.9	461	4	US-09-800-909-2	Sequence 2, Appli
34	305	26.9	461	4	US-09-758-124-2	Sequence 2, Appli
35	305	26.9	461	4	US-09-800-908-3	Sequence 3, Appli
36	305	26.9	461	6	5395760-2	Patent No. 5395760
37	305	26.9	486	1	US-08-243-010-1	Sequence 1, Appli
38	305	26.9	518	1	US-08-385-229-4	Sequence 4, Appli
39	305	26.9	518	4	US-09-579-845-1	Sequence 1, Appli
40	305	26.9	518	4	US-09-579-845-3	Sequence 1, Appli
41	304	26.8	235	4	US-09-580-235-4	Sequence 4, Appli
42	304	26.8	235	4	US-09-580-235-6	Sequence 4, Appli
43	304	26.8	235	4	US-09-580-181-4	Sequence 6, Appli
44	304	26.8	235	4	US-09-580-181-6	Sequence 6, Appli
45	304	26.8	235	4	US-09-102-530-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-505-606-1
; Sequence 1, Application US/08505606
; Patent No. 5925351
; GENERAL INFORMATION:
; APPLICANT: BROWNING, Jeffrey L.
; APPLICANT: BENJAMIN, Christopher D.
; APPLICANT: HOCHMAN, Paula S.
; TITLE OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTORS AND
; TITLE OF INVENTION: ANTI-LYMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS
; TITLE OF INVENTION: THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL
; DISEASE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr.
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,606
; FILING DATE: 21-JUL-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378,968
; FILING DATE: 26-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B191
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-505-606-1
Query Match 100.0%; Score 1133; DB 2; Length 197;

Best Local Similarity 100.0%; Pred. No. 2.5e-99;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOPAVPPYASENCTCRDOEKEYEPOHRIICSRCPGTIVYSAKCSRIRDTVCATCAENS 60
Db 1 SOPAVPPYASENCTCRDOEKEYEPOHRIICSRCPGTIVYSAKCSRIRDTVCATCAENS 60

QY 61 YNEHNNYLTICQLCRPCDPVWGLEIAFCTSKRTQCGCPGMFCAMALECTHCELLSD 120
Db 61 YNEHNNYLTICQLCRPCDPVWGLEIAFCTSKRTQCGCPGMFCAMALECTHCELLSD 120

QY 121 CPPTGTEALKDEVGKNNHCVPCKAGHPONTSSPSARCOPTHRCNOGLVEAAPGTAOSD 180
Db 121 CPPTGTEALKDEVGKNNHCVPCKAGHPONTSSPSARCOPTHRCNOGLVEAAPGTAOSD 180

QY 181 TTCKNPLEPLPPEMSGT 197
Db 181 TTCKNPLEPLPPEMSGT 197

RESULT 2

US-09-000-166-1
Sequence 1, Application US/09000166A
Patent No. 6403087
GENERAL INFORMATION:
APPLICANT: BROWNING, et al.
TITLE OF INVENTION: Soluble Lymphotoxin-B Receptors and Anti-Lymphotoxin
TITLE OF INVENTION: Receptor and Ligand Antibodies, as Therapeutic Agents
TITLE OF INVENTION: for the Treatment of Immunological Disease.
FILE REFERENCE: B191
CURRENT APPLICATION NUMBER: US/09/000,166A
CURRENT FILING DATE: 1998-06-08
EARLIER APPLICATION NUMBER: PCT/US96/12010
EARLIER FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 197
TYPE: PRT
ORGANISM: Homo sapiens
US-09-000-166-1

Query Match 100.0%; Score 1133; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.5e-99;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOPAVPPYASENCTCRDOEKEYEPOHRIICSRCPGTIVYSAKCSRIRDTVCATCAENS 60
Db 1 SOPAVPPYASENCTCRDOEKEYEPOHRIICSRCPGTIVYSAKCSRIRDTVCATCAENS 60

QY 61 YNEHNNYLTICQLCRPCDPVWGLEIAFCTSKRTQCGCPGMFCAMALECTHCELLSD 120
Db 61 YNEHNNYLTICQLCRPCDPVWGLEIAFCTSKRTQCGCPGMFCAMALECTHCELLSD 120

QY 121 CPPTGTEALKDEVGKNNHCVPCKAGHPONTSSPSARCOPTHRCNOGLVEAAPGTAOSD 180
Db 121 CPPTGTEALKDEVGKNNHCVPCKAGHPONTSSPSARCOPTHRCNOGLVEAAPGTAOSD 180

QY 181 TTCKNPLEPLPPEMSGT 197
Db 181 TTCKNPLEPLPPEMSGT 197

RESULT 3

US-09-303-262-1
Sequence 1, Application US/09303262
Patent No. 6669941
GENERAL INFORMATION:
APPLICANT: BROWNING, Jeffrey L.
HUCHMAN, Christopher D.
TITLE OF INVENTION: SOLUBLE LYMPHOTOXIN-BETA RECEPTOR AND LIGAND ANTIBODIES AS
ANTI-LYMPHOTOXIN RECEPTOR AND LIGAND ANTIBODIES AS

THERAPEUTIC AGENTS FOR THE TREATMENT OF IMMUNOLOGICAL DISEASE

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr.
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,262
FILING DATE: 30-Apr-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/505,606
FILING DATE: 21-Jul-1995
APPLICATION NUMBER: US 08/378,968
FILING DATE: 26-Jan-1995
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B191
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-303-262-1

Query Match 100.0%; Score 1133; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.5e-99;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOPAVPPYASENCTCRDOEKEYEPOHRIICSRCPGTIVYSAKCSRIRDTVCATCAENS 60
Db 1 SOPAVPPYASENCTCRDOEKEYEPOHRIICSRCPGTIVYSAKCSRIRDTVCATCAENS 60

QY 61 YNEHNNYLTICQLCRPCDPVWGLEIAFCTSKRTQCGCPGMFCAMALECTHCELLSD 120
Db 61 YNEHNNYLTICQLCRPCDPVWGLEIAFCTSKRTQCGCPGMFCAMALECTHCELLSD 120

QY 121 CPPTGTEALKDEVGKNNHCVPCKAGHPONTSSPSARCOPTHRCNOGLVEAAPGTAOSD 180
Db 121 CPPTGTEALKDEVGKNNHCVPCKAGHPONTSSPSARCOPTHRCNOGLVEAAPGTAOSD 180

QY 181 TTCKNPLEPLPPEMSGT 197
Db 181 TTCKNPLEPLPPEMSGT 197

RESULT 4

US-08-828-683A-14
Sequence 14, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 L1 AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

```
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Winpatin (Genentech)
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/828,683A
/ FILING DATE: 31-Mar-1997
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/625328
/ FILING DATE: 1-Apr-1996
/ APPLICATION NUMBER: 08/710802
/ FILING DATE: 23-Sep-1996
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Marschang, Diane L.
/ REGISTRATION NUMBER: 35,600
/ REFERENCE/DOCKET NUMBER: P1007P1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-5416
/ TELEFAX: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 14:
/
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 170 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-828-683A-14
Query Match      87.1%; Score 987; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-85;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 TCDDQKEYEYEPHRIICCSRCPPGTIVYSAKCSIRPTVCATCAENSYNEHMYLTICQLC 60
QY 75 RPDDPYMGLEIAPCTSKRTQCRCPGMFCAMALECTHCELLSDCPPTAELELDEVG 134
DB 61 RPDDPYMGLEIAPCTSKRTQCRCPGMFCAMALECTHCELLSDCPPTAELELDEVG 120
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DB 121 KANNHCVPCKAGHFONTSSPSARCOPHTRCENOGIVEAARPTAQSPTTCK 170
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/ RESULT 5
/ US-09-523-323-57
/ Sequence 57, Application US/09523323
/ Patent No. 6635743
/ GENERAL INFORMATION:
/ APPLICANT: Edner, Reinhard
/ APPLICANT: Yu, Guo-Liang
/ APPLICANT: Ruben, Steven M.
/ APPLICANT: Ulrich, Stephen
/ APPLICANT: Zhai, Yifan
/ TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
/ FILE REFERENCE: 1488,065000C
/ CURRENT APPLICATION NUMBER: US/09/523,323
/ EARLIER FILING DATE: 2000-03-10
/ EARLIER APPLICATION NUMBER: 60/168,380
/ EARLIER FILING DATE: 1999-12-02
/ EARLIER APPLICATION NUMBER: 60/148,326
/ EARLIER FILING DATE: 1999-08-11
/ EARLIER APPLICATION NUMBER: 60/142,657
/ EARLIER FILING DATE: 1999-07-06
/ EARLIER APPLICATION NUMBER: 60/137,457
/ EARLIER FILING DATE: 1999-06-04
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/ EARLIER APPLICATION NUMBER: 60/124,041
/ EARLIER FILING DATE: 1999-03-11
/ EARLIER APPLICATION NUMBER: 09/252,656
/ EARLIER FILING DATE: 1999-02-19
/ EARLIER APPLICATION NUMBER: 60/075,409
/ EARLIER FILING DATE: 1998-02-20
/ EARLIER APPLICATION NUMBER: 09/027,287
/ EARLIER FILING DATE: 1998-02-20
/ EARLIER APPLICATION NUMBER: 09/003,886
/ EARLIER FILING DATE: 1998-01-07
/ EARLIER APPLICATION NUMBER: 08/822,953
/ EARLIER FILING DATE: 1997-03-21
/ EARLIER APPLICATION NUMBER: 60/013,923
/ EARLIER FILING DATE: 1996-03-22
/ EARLIER APPLICATION NUMBER: 60/030,157
/ EARLIER FILING DATE: 1996-10-31
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 57
/ LENGTH: 170
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (7)
/ OTHER INFORMATION: May be any amino acid
/ US-09-523-323-57
Query Match      86.6%; Score 981; DB 4; Length 170;
Best Local Similarity 99.4%; Pred. No. 4.3e-85;
Matches 169; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 TCDDQKEYEYEPHRIICCSRCPPGTIVYSAKCSIRPTVCATCAENSYNEHMYLTICQLC 74
DB 1 TCDDQKEYEYEPHRIICCSRCPPGTIVYSAKCSIRPTVCATCAENSYNEHMYLTICQLC 60
QY 75 RPDDPYMGLEIAPCTSKRTQCRCPGMFCAMALECTHCELLSDCPPTAELELDEVG 134
DB 61 RPDDPYMGLEIAPCTSKRTQCRCPGMFCAMALECTHCELLSDCPPTAELELDEVG 120
QY 135 KANNHCVPCKAGHFONTSSPSARCOPHTRCENOGIVEAARPTAQSPTTCK 184
DB 121 KANNHCVPCKAGHFONTSSPSARCOPHTRCENOGIVEAARPTAQSPTTCK 170
/
/ RESULT 6
/ US-09-006-353A-6
/ Sequence 6, Application US/09006353A
/ Patent No. 6261801
/ GENERAL INFORMATION:
/ APPLICANT: WEI, YING-FEI
/ APPLICANT: YU, GUO-LIANG
/ APPLICANT: GENTZ, REINER
/ APPLICANT: RUBEN, STEVEN
/ TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: HUMAN GENOME SCIENCES, INC.
/ STREET: 9410 KEY WEST AVENUE
/ CITY: ROCKVILLE
/ STATE: MD
/ COUNTRY: US
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/006,353A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
```

NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF341
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-006-353A-6

Query Match 68.0%; Score 771; DB 3; Length 415;
Best Local Similarity 70.7%; Pred. No. 7.1e-65;
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

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DB 28 SGPQLVPPYRIENQTCWDQKEYEYEPMDVCCSRCPGEFFAVCSRSODTVCKTCPEHNS 87
QY 61 YNEHNNVLTICQLCRPCDPVWGIEIAPCTSKRTQCRQCPGMFCAMALECTHC--ELL 118
DB 88 YNEHNNHLSLTCQLCRPCDVLGFEFVAPCTSDRAECRCQPGMFCVYLNECVHCEBERL 147
QY 119 SDPCPGTEALKDEVGKNNHCVPCKAGHFONTSSPSARCOPTHRCENOGIVEAAPGTAQ 178
DB 148 VLCQPGTEAEVATDMDTVNVCVCKPGHFONTSSPSARCOPTHRCETIQLGVEAAPGTSY 207
QY 179 SDTCKNPLEP 189
DB 208 SDTCKNPPPEP 218

RESULT 7
US-09-573-986-6
Sequence 6, Application US/09573986
Patent No. 6455040
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Ni, Jien
APPLICANT: Genz, Reiner
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.1280004
CURRENT APPLICATION NUMBER: US/09/573,986
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 6
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
US-09-573-986-6

Query Match 68.0%; Score 771; DB 4; Length 415;
Best Local Similarity 70.7%; Pred. No. 7.1e-65;
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SGPQAVPPVASENQTCDQEKYEYEPQHRICCSRCPPGTIVSAKCSRIKDTVCATCAENS 60
DB 28 SGPQLVPPYRIENQTCWDQKEYEYEPMDVCCSRCPGEFFAVCSRSODTVCKTCPEHNS 87
QY 61 YNEHNNVLTICQLCRPCDPVWGIEIAPCTSKRTQCRQCPGMFCAMALECTHC--ELL 118
DB 88 YNEHNNHLSLTCQLCRPCDVLGFEFVAPCTSDRAECRCQPGMFCVYLNECVHCEBERL 147
QY 119 SDPCPGTEALKDEVGKNNHCVPCKAGHFONTSSPSARCOPTHRCENOGIVEAAPGTAQ 178
DB 148 VLCQPGTEAEVATDMDTVNVCVCKPGHFONTSSPSARCOPTHRCETIQLGVEAAPGTSY 207

QY 179 SDTCKNPLEP 189
DB 208 SDTCKNPPPEP 218

RESULT 8
US-08-866-545-3
Sequence 3, Application US/08866545
Patent No. 626535
GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
APPLICANT: Muraki, Ramachandran
APPLICANT: Takasaki, Wataru
TITLE OF INVENTION: PEPTIDES AND PEPTIDE
TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,545
FILING DATE: 30-MAY-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009113-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-5556
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 626535e
US-08-866-545-3

Query Match 40.2%; Score 456; DB 3; Length 77;
Best Local Similarity 100.0%; Pred. No. 5.1e-36;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNEHNNVLTICQLCRPCDPVWGIEIAPCTSKRTQCRQCPGMFCAMALE 111
DB 1 VCATCAENSYNEHNNVLTICQLCRPCDPVWGIEIAPCTSKRTQCRQCPGMFCAMALE 60
QY 112 CTHCELLSDCPGTEAE 128
DB 61 CTHCELLSDCPGTEAE 77

RESULT 9
US-09-627-775-3
Sequence 3, Application US/09627775
Patent No. 6682739
GENERAL INFORMATION:
APPLICANT: Greene, Mark

APPLICANT: Murali, Ramachandran
APPLICANT: Aoki, Kazuhiko
APPLICANT: Baron, Roland
TITLE OF INVENTION: Methods of Inhibiting Osteoclastogenesis
FILE REFERENCE: UPN3832
CURRENT APPLICATION NUMBER: US/09/627,775
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/146,090
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
US-09-627-775-3

Query Match 40.2%; Score 456; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 5, 1e-36;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNEHNYLTICQLCPDPPVNGLEBIAPCTSKRTQCRQCPGMCAWALE 111
DB 1 VCATCAENSYNEHNYLTICQLCPDPPVNGLEBIAPCTSKRTQCRQCPGMCAWALE 60
QY 112 CTRCELLSDCPPTGEAE 128
DB 61 CTRCELLSDCPPTGEAE 77

RESULT 10
US-08-974-022-48
Sequence 48, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Mang-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehaviiland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-48

Query Match 26.9%; Score 305; DB 3; Length 227;

Best Local Similarity 35.0%; Pred. No. 2, 8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
QY 5 AVPPYASE-NQTCRDOEKEYEYEPQHRICSCRCPPGTIVYSAKCSRIIDTVATCAENSYNE 63
DB 28 AVPPYASEPSTGR--LREYDQTAQWCKSCSPQAHKVPCTKSDTVCSCEBSTDYQ 85
QY 64 HNNYLTICQLCR--PCDPVNGLEBIAPCTSKRTQCRQCPGMCAWALE-CTRCELLS 119
DB 86 LNNVPECLSCGSRCSQV---ETQACTREQRICITCRPGWYCALSKQEGCRLCAPLR 141
QY 120 DCPPG-----TEAPLDEVKGNHVCYPCAGHPONTSPSPARCQHTRENOGLVDAAP 174
DB 142 KCRPFGVAPRGTSIDVV-----CKPCAPGTFTNTSSSTDICRPHQICN---VVAIP 191
QY 175 GTAQSDPTTC--KNPLEPLPP 192
DB 192 GNASRDVAVCTISPTSRMAP 211

RESULT 11
US-08-795-445A-48
Sequence 48, Application US/08795445A
Patent No. 6284485
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Mang-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehaviiland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-445A-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 2, 8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPYASE-NQTCRDOEKEYEYEPQHRICSCRCPPGTIVYSAKCSRIIDTVATCAENSYNE 63
DB 28 AVPPYASEPSTGR--LREYDQTAQWCKSCSPQAHKVPCTKSDTVCSCEBSTDYQ 85
QY 64 HNNYLTICQLCR--PCDPVNGLEBIAPCTSKRTQCRQCPGMCAWALE-CTRCELLS 119
DB 86 LNNVPECLSCGSRCSQV---ETQACTREQRICITCRPGWYCALSKQEGCRLCAPLR 141

STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winer, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 227 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-446B-48

Query Match 26.9%; Score 305; DB 3; Length 227;
Best Local Similarity 35.0%; Pred. No. 2.8e-21;

Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPYASE-NOTGRDQKEYEPEQHRICRCRPPGTIVSAKCSRIIDTVCAATCAENSYNE 63
DB 28 AFPPYAPEPSTCR--LREYYDQTAQWCCSKSPGQAKVFCRTKSTDTVCDCSCEDSTYTQ 85
QY 64 HMYVLTICQLCR---PCDDPYMGLBEIAPCTSKRTQCRQCPMGFCAMALE-CTHCELLS 119
DB 86 LMMWVECLSCGSRCSDDV---ETQACTREONRICTCRPGWCALSKQEGCRLCAPLR 141
QY 120 DCEPG-----TEALKDEVGKNNHCVPCKAGHONTSSPARCOPHTRCENGLVEAP 174
DB 142 KCRPGGVARPGTETSDV-----CKPCAPGTFSNTSTSDICRPHQICN---VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
DB 192 GNASRDVACTSTSPTRMAP 211

RESULT 15

US-08-706-945D-134
Sequence 134, Application US/08706945D
Patent No. 6369027
GENERAL INFORMATION:
APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Calzone, Frank
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patentn version 3.1
SEQ ID NO 134
LENGTH: 227
TYPE: prt
ORGANISM: Homo sapiens
US-08-706-945D-134

Query Match 26.9%; Score 305; DB 4; Length 227;
Best Local Similarity 35.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;

QY 5 AVPPYASE-NOTGRDQKEYEPEQHRICRCRPPGTIVSAKCSRIIDTVCAATCAENSYNE 63
DB 28 AFPPYAPEPSTCR--LREYYDQTAQWCCSKSPGQAKVFCRTKSTDTVCDCSCEDSTYTQ 85
QY 64 HMYVLTICQLCR---PCDDPYMGLBEIAPCTSKRTQCRQCPMGFCAMALE-CTHCELLS 119
DB 86 LMMWVECLSCGSRCSDDV---ETQACTREONRICTCRPGWCALSKQEGCRLCAPLR 141
QY 120 DCEPG-----TEALKDEVGKNNHCVPCKAGHONTSSPARCOPHTRCENGLVEAP 174
DB 142 KCRPGGVARPGTETSDV-----CKPCAPGTFSNTSTSDICRPHQICN---VVAIP 191
QY 175 GTAQSDTTC--KNPLEPLPP 192
DB 192 GNASRDVACTSTSPTRMAP 211

Search completed: August 27, 2004, 21:11:47
Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 27, 2004, 21:10:31 ; Search time 124 Seconds

(without alignments)
499.829 Million cell updates/sec

Title: US-09-626-219-1

Perfect score: 1133
Sequence: 1 SQFOAVPPYASENQCRDQF.....QSDTCKNPLEPLPMSGRT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 1297172

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications AA:*
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3: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*
5: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*
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17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1133	100.0	197	13	US-10-003-211-1
2	1133	100.0	435	9	US-09-907-372-19
3	1133	100.0	435	9	US-09-768-779A-6
4	1133	100.0	435	10	US-09-917-372-19
5	1133	100.0	435	12	US-10-087-192-942
6	1133	100.0	435	14	US-10-291-480-6
7	1133	100.0	435	15	US-10-369-300-17
8	1133	100.0	435	15	US-10-262-445-133
9	1129	99.6	399	9	US-09-907-372-1
10	1129	99.6	399	10	US-09-917-372-1
11	987	87.1	170	13	US-10-112-793-14
12	970	85.6	172	15	US-10-375-680-57
13	780	68.8	257	9	US-09-948-018-19
14	771	68.0	402	12	US-10-087-192-939
15	771	68.0	415	9	US-09-826-212-6

16	771	68.0	415	9	US-09-907-372-20	Sequence 20, Appl
17	771	68.0	415	9	US-09-935-727-8	Sequence 8, Appl
18	771	68.0	415	10	US-09-917-372-20	Sequence 20, Appl
19	771	68.0	415	14	US-10-186-643-6	Sequence 6, Appl
20	771	68.0	415	15	US-10-418-242-8	Sequence 8, Appl
21	381.5	33.7	305	15	US-10-264-049-3058	Sequence 3058, Ap
22	311.5	27.5	659	14	US-10-363-427-12	Sequence 12, Appl
23	307	27.1	720	14	US-10-363-427-8	Sequence 8, Appl
24	305	26.9	225	9	US-09-840-795-10	Sequence 10, Appl
25	305	26.9	227	11	US-09-405-032-131	Sequence 131, App
26	305	26.9	235	9	US-09-907-263-4	Sequence 4, Appl
27	305	26.9	235	10	US-09-882-735-16	Sequence 16, Appl
28	305	26.9	235	12	US-10-621-783-4	Sequence 4, Appl
29	305	26.9	235	12	US-10-622-383-4	Sequence 4, Appl
30	305	26.9	235	14	US-10-243-230-2	Sequence 2, Appl
31	305	26.9	235	14	US-10-243-230-8	Sequence 8, Appl
32	305	26.9	225	14	US-10-436-826-75	Sequence 75, Appl
33	305	26.9	257	14	US-10-313-852-10	Sequence 10, Appl
34	305	26.9	257	14	US-10-314-033-10	Sequence 10, Appl
35	305	26.9	439	15	US-10-360-101-226	Sequence 226, App
36	305	26.9	450	9	US-09-768-779A-3	Sequence 3, Appl
37	305	26.9	450	14	US-10-291-480-3	Sequence 3, Appl
38	305	26.9	451	9	US-09-800-909-2	Sequence 2, Appl
39	305	26.9	451	9	US-09-826-212-4	Sequence 4, Appl
40	305	26.9	451	9	US-09-758-124-2	Sequence 2, Appl
41	305	26.9	451	9	US-09-896-096A-17	Sequence 17, Appl
42	305	26.9	451	9	US-09-894-924-17	Sequence 17, Appl
43	305	26.9	451	9	US-09-840-907A-17	Sequence 17, Appl
44	305	26.9	451	9	US-09-800-908-3	Sequence 3, Appl
45	305	26.9	451	9	US-09-935-727-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-003-211-1
Sequence 1, Application US/10003211
Publication No. US20020197254A1
GENERAL INFORMATION:
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: Soluble Lymphotoxin Beta Receptor and Anti-Lymphotoxin Receptor and Ligand Antibodies as
TITLE OF INVENTION: Therapeutic Agents for the Treatment of Immunological
FILE REFERENCE: A013US
CURRENT APPLICATION NUMBER: US/10/003,211
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: PCT/US97/19436
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/029,060
PRIOR FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 197
TYPE: PRT
ORGANISM: Homo Sapien
US-10-003-211-1

Query Match 100.0%; Score 1133; DB 13; Length 197;
Best Local Similarity 100.0%; Pred. No. 7.6e-89;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	SQFOAVPPYASENQCRDQFVGHIEETAPCTSRKTKQRCQPGWFCAMALTECHGELSD	60
DB	1	SQFOAVPPYASENQCRDQFVGHIEETAPCTSRKTKQRCQPGWFCAMALTECHGELSD	60
QY	61	YNEHMYLITICQCRPDQVVGIEETAPCTSRKTKQRCQPGWFCAMALTECHGELSD	120
DB	61	YNEHMYLITICQCRPDQVVGIEETAPCTSRKTKQRCQPGWFCAMALTECHGELSD	120

QY 121 CPPTGEALKDEYKGNHNCVPCAGHFONTSSPASCQPHTRCENGLVEAAGTAQSD 180
DB 121 CPPTGEALKDEYKGNHNCVPCAGHFONTSSPASCQPHTRCENGLVEAAGTAQSD 180
QY 181 TTCKNPLEPLPEMSGT 197
DB 181 TTCKNPLEPLPEMSGT 197

RESULT 2
US-09-907-372-19
Sequence 19, Application US/09907372
Patent No. US20020068242A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti G.
APPLICANT: Warren, Bridget A.
TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
FILE REFERENCE: PC-0050 US
CURRENT APPLICATION NUMBER: US/09/907,372
CURRENT FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO 19
LENGTH: 435
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020068242A1 g339762
US-09-907-372-19

Query Match 100.0%; Score 1133; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 1,7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOPQAVPPYASENCTCRDQEKYEYEPQHRICCSRCPPTGYVSACSRIRDTVCATCAENS 60
DB 28 SOPQAVPPYASENCTCRDQEKYEYEPQHRICCSRCPPTGYVSACSRIRDTVCATCAENS 87
QY 61 YNEHNNVLTTCQLCRPCDPVWGLEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 120
DB 88 YNEHNNVLTTCQLCRPCDPVWGLEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 147
QY 121 CPPTGEALKDEYKGNHNCVPCAGHFONTSSPASCQPHTRCENGLVEAAGTAQSD 180
DB 148 CPPTGEALKDEYKGNHNCVPCAGHFONTSSPASCQPHTRCENGLVEAAGTAQSD 207
QY 181 TTCKNPLEPLPEMSGT 197
DB 208 TTCKNPLEPLPEMSGT 224

RESULT 3
US-09-768-779A-6
Sequence 6, Application US/09768779A
Patent No. US20020127637A1
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: MOORE, PAUL
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR
RECEPTOR-LIKE PROTEIN 8
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/768,779A
FILING DATE: 25-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/086,582
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: KENLEY K. HOOVER
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: P366PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-768-779A-6

Query Match 100.0%; Score 1133; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 1,7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOPQAVPPYASENCTCRDQEKYEYEPQHRICCSRCPPTGYVSACSRIRDTVCATCAENS 60
DB 28 SOPQAVPPYASENCTCRDQEKYEYEPQHRICCSRCPPTGYVSACSRIRDTVCATCAENS 87
QY 61 YNEHNNVLTTCQLCRPCDPVWGLEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 120
DB 88 YNEHNNVLTTCQLCRPCDPVWGLEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 147
QY 121 CPPTGEALKDEYKGNHNCVPCAGHFONTSSPASCQPHTRCENGLVEAAGTAQSD 180
DB 148 CPPTGEALKDEYKGNHNCVPCAGHFONTSSPASCQPHTRCENGLVEAAGTAQSD 207
QY 181 TTCKNPLEPLPEMSGT 197
DB 208 TTCKNPLEPLPEMSGT 224

RESULT 4
US-09-917-372-19
Sequence 19, Application US/09917372
Patent No. US20030068619A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti G.
APPLICANT: Warren, Bridget A.
TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
FILE REFERENCE: PC-0050 US
CURRENT APPLICATION NUMBER: US/09/917,372
CURRENT FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO 19
LENGTH: 435
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030068619A1 g339762
US-09-917-372-19

Query Match 100.0%; Score 1133; DB 10; Length 435;
Best Local Similarity 100.0%; Pred. No. 1,7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOPQAVPPYASENCTCRDQEKYEYEPQHRICCSRCPPTGYVSACSRIRDTVCATCAENS 60

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DB 28 SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTIVYSAKCSRIKDTVCATCAENS 87
QY 61 YNEHNNYLTTCQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
DB 88 YNEHNNYLTTCQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 147
QY 121 CPPTGEALKDDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 180
DB 148 CPPTGEALKDDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 207
QY 181 TTCNNPLEPLPEMSGT 197
DB 208 TTCNNPLEPLPEMSGT 224
```

RESULT 5

```
US-10-087-192-942
; Sequence 942, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 942
; LENGTH: 435
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-087-192-942
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```
Query Match 100.0%; Score 1133; DB 12; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTIVYSAKCSRIKDTVCATCAENS 60
DB 28 SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTIVYSAKCSRIKDTVCATCAENS 87
QY 61 YNEHNNYLTTCQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
DB 88 YNEHNNYLTTCQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 147
QY 121 CPPTGEALKDDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 180
DB 148 CPPTGEALKDDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 207
QY 181 TTCNNPLEPLPEMSGT 197
DB 208 TTCNNPLEPLPEMSGT 224
```

RESULT 6

```
US-10-291-480-6
; Sequence 6, Application US/10291480
; Publication No. US20030100069A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Moore, Paul
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Protein 8
; FILE REFERENCE: P3368C1D1
; CURRENT APPLICATION NUMBER: US/10/291,480
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/766,779
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; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/086,582
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/048,020
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 435
; TYPE: PR
; ORGANISM: human
US-10-291-480-6
```

```
Query Match 100.0%; Score 1133; DB 14; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTIVYSAKCSRIKDTVCATCAENS 60
DB 28 SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTIVYSAKCSRIKDTVCATCAENS 87
QY 61 YNEHNNYLTTCQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
DB 88 YNEHNNYLTTCQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 147
QY 121 CPPTGEALKDDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 180
DB 148 CPPTGEALKDDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 207
QY 181 TTCNNPLEPLPEMSGT 197
DB 208 TTCNNPLEPLPEMSGT 224
```

RESULT 7

```
US-10-369-300-17
; Sequence 17, Application US/10369300
; Publication No. US20030215442A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher
; APPLICANT: Hancock, Wayne
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
; FILE REFERENCE: 7853-255
; CURRENT APPLICATION NUMBER: US/10/369,300
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/358,463
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 435
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-369-300-17
```

```
Query Match 100.0%; Score 1133; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTIVYSAKCSRIKDTVCATCAENS 60
DB 28 SGPQAVPPYASENOTCRDQEKYEYEPQHRICCSRCPGTIVYSAKCSRIKDTVCATCAENS 87
QY 61 YNEHNNYLTTCQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
DB 88 YNEHNNYLTTCQLCRPCDPVWGLBEIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 147
QY 121 CPPTGEALKDDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 180
DB 148 CPPTGEALKDDEVGKGNHCVPCAKGHFQNTSSPSARCQPHTRCENOGIVEAARGTASD 207
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QY 181 TTCKNPLEPLPEMSGT 197
DB 208 TTCKNPLEPLPEMSGT 224

RESULT 8

US-10-262-445-133
; Sequence 133, Application US/10262445
; Publication No. US20040014058A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Carterton, Elina
; APPLICANT: Chant, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Giot, Loic
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Mezes, Peter
; APPLICANT: Millet, Isabelle
; APPLICANT: Ooi, Chean Eng
; APPLICANT: Paturajan, Meera
; APPLICANT: Rieger, Daniel
; APPLICANT: Spylek, Kimberly
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Zernusen, Bryan
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS C
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 21402-462D
; CURRENT APPLICATION NUMBER: US/10/262,445
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/327,454
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/327,917
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,029
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,056
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/328,849
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/329,414
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/330,142
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/341,058
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/343,629
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 60/349,575
; PRIOR FILING DATE: 2001-10-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: CuroSeqLast version 0.1
; SEQ ID NO 133
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-445-133

Query Match 100.0%; Score 1133; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.7e-88;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGPQAVPPYASENQCRDQEKYEYEPQHRICCSRCPCPGTYVSACKSRIRDYTCATCAENS 60
DB 28 SGPQAVPPYASENQCRDQEKYEYEPQHRICCSRCPCPGTYVSACKSRIRDYTCATCAENS 87

QY 61 YNEHNNYLTICQLCRPCDPVNGLEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSD 120
DB 88 YNEHNNYLTICQLCRPCDPVNGLEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSD 147
QY 121 CPGTEALKDQEVGKGNHCVPCXAGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAOSD 180
DB 148 CPGTEALKDQEVGKGNHCVPCXAGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAOSD 207
QY 181 TTCKNPLEPLPEMSGT 197
DB 208 TTCKNPLEPLPEMSGT 224

RESULT 9

US-09-907-372-1
; Sequence 1, Application US/09907372
; Patent No. US20020068242A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/907,372
; CURRENT FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020068242A1 7497867CD1
US-09-907-372-1

Query Match 99.6%; Score 1129; DB 9; Length 399;
Best Local Similarity 99.5%; Pred. No. 3.5e-88;
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGPQAVPPYASENQCRDQEKYEYEPQHRICCSRCPCPGTYVSACKSRIRDYTCATCAENS 60
DB 28 SGPQAVPPYASENQCRDQEKYEYEPQHRICCSRCPCPGTYVSACKSRIRDYTCATCAENS 87
QY 61 YNEHNNYLTICQLCRPCDPVNGLEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSD 120
DB 88 YNEHNNYLTICQLCRPCDPVNGLEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSD 147
QY 121 CPGTEALKDQEVGKGNHCVPCXAGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAOSD 180
DB 148 CPGTEALKDQEVGKGNHCVPCXAGHFQNTSSPSARCQPHTRCENOGIVEAAPGTAOSD 207
QY 181 TTCKNPLEPLPEMSGT 197
DB 208 TTCKNPLEPLPEMSGT 224

RESULT 10

US-09-917-372-1
; Sequence 1, Application US/09917372
; Publication No. US20030068619A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti G.
; APPLICANT: Warren, Bridget A.
; TITLE OF INVENTION: TNF RECEPTOR 2 RELATED PROTEIN VARIANT
; FILE REFERENCE: PC-0050 US
; CURRENT APPLICATION NUMBER: US/09/917,372
; CURRENT FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens

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FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030068619A1 7497867CD1
US-09-917-372-1
Query Match      99.6%; Score 1129; DB 10; Length 399;
Best Local Similarity 99.5%; Pred. No. 3.5e-86;
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQGAVPPYASENQTCRDQEXEYEPQHRICCSRPPTYVSACSRIIDTVCAATCAENS 60
   |||||
Db 28 SQGAVPPYASENQTCRDQEXEYEPQHRICCSRPPTYVSACSRIIDTVCAATCAENS 87
   |||||
QY 61 YNEHNNYLTITICQLCRPCDPVWGLEIAPCTSKRTQCRQGMFCAAMALECTHCELLSD 120
   |||||
Db 88 YNEHNNYLTITICQLCRPCDPVWGLEIAPCTSKRTQCRQGMFCAAMALECTHCELLSD 147
   |||||
QY 121 CPGTEALKDQEVGKNNHCVPCKAGHFQNTSSPSARQCPHTRCENQGLVEAPGTAOSDTTCK 180
   |||||
Db 148 CPGTEALKDQEVGKNNHCVPCKAGHFQNTSSPSARQCPHTRCENQGLVEAPGTAOSDTTCK 207
   |||||
QY 181 TTCNPLEPLPEMMSGT 197
   |||||
Db 208 TTCNPLEPLPEMMSGS 224
   |||||

RESULT 11
US-10-112-793-14
; Sequence 14, Application US/10112793
; Publication No. US20020192729A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 170 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-112-793-14
Query Match      87.1%; Score 987; DB 13; Length 170;

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Best Local Similarity 100.0%; Pred. No. 1.9e-76;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TCRDQEXEYEPQHRICCSRCPPPTYVSACSRIIDTVCAATCAENS YNEHNNYLTITICQLC 74
   |||||
Db 1 TCRDQEXEYEPQHRICCSRCPPPTYVSACSRIIDTVCAATCAENS YNEHNNYLTITICQLC 60
   |||||
QY 75 RPCDPVWGLEIAPCTSKRTQCRQGMFCAAMALECTHCELLSDCPGTEALKDQEVG 134
   |||||
Db 61 RPCDPVWGLEIAPCTSKRTQCRQGMFCAAMALECTHCELLSDCPGTEALKDQEVG 120
   |||||
QY 135 KGNHHCVPCKAGHFQNTSSPSARQCPHTRCENQGLVEAPGTAOSDTTCK 184
   |||||
Db 121 KGNHHCVPCKAGHFQNTSSPSARQCPHTRCENQGLVEAPGTAOSDTTCK 170
   |||||

RESULT 12
US-10-375-680-57
; Sequence 57, Application US/10375680
; Publication No. US20040009147A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1488,065000E
; CURRENT APPLICATION NUMBER: US/10/375,680
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,234
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7)-(17)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-375-680-57
Query Match      85.6%; Score 970; DB 15; Length 172;
Best Local Similarity 98.3%; Pred. No. 5.3e-75;
Matches 169; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 15 TCRDQE--KEYEPQHRICCSRCPPPTYVSACSRIIDTVCAATCAENS YNEHNNYLTITICQ 72
   |||||
Db 1 TCRDQEXAAEYEPQHRICCSRCPPPTYVSACSRIIDTVCAATCAENS YNEHNNYLTITICQ 60
   |||||
QY 73 LCRPCDPVWGLEIAPCTSKRTQCRQGMFCAAMALECTHCELLSDCPGTEALKDQEVG 132
   |||||
Db 61 LCRPCDPVWGLEIAPCTSKRTQCRQGMFCAAMALECTHCELLSDCPGTEALKDQEVG 120
   |||||
QY 133 VGGKNNHCVPCKAGHFQNTSSPSARQCPHTRCENQGLVEAPGTAOSDTTCK 184
   |||||
Db 121 VGGKNNHCVPCKAGHFQNTSSPSARQCPHTRCENQGLVEAPGTAOSDTTCK 172
   |||||

RESULT 13
US-09-948-018-19
; Sequence 19, Application US/09948018
; Patent No. US20020150977A1
; GENERAL INFORMATION:
; APPLICANT: Theill et al
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37677
; CURRENT APPLICATION NUMBER: US/09/948,018
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,191
; PRIOR FILING DATE: 2000-09-05

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NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 257
TYPE: PRT
ORGANISM: Mus musculus
US-09-948-018-19

Query Match 68.8%; Score 780; DB 9; Length 257;
Best Local Similarity 100.0%; Pred. No. 1,3e-58;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 EHMNYLTICQLCRPCDPVWGIEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSDCP 122
DB 1 EHMNYLTICQLCRPCDPVWGIEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSDCP 60
QY 123 PGTAEELKDEYKGNHCVCKAGHFONTSSPSARCPHTRCENQGLVEAAPGTASDTT 182
DB 61 PGTAEELKDEYKGNHCVCKAGHFONTSSPSARCPHTRCENQGLVEAAPGTASDTT 120
QY 183 CKNPLEPPPEMSGT 197
DB 121 CKNPLEPPPEMSGT 135

RESULT 14

US-10-087-192-939
Sequence 939, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 939
LENGTH: 402
TYPE: PRT
ORGANISM: Mus musculus
US-10-087-192-939

Query Match 68.0%; Score 771; DB 12; Length 402;
Best Local Similarity 70.7%; Pred. No. 1.2e-57;
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTIVYSAKCSRIIDTVCATCAENS 60
DB 41 SQPQAVPPYRIENQTCWQDQKEYEYEPMDVCCSCPPGEFVAVCSRSQDITVCKTCPHNS 100
QY 61 YNEHMNYLTICQLCRPCDPVWGIEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSDCP 118
DB 101 YNEHMNYLTICQLCRPCDPVWGIEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSDCP 160
QY 119 SDCCPTEAEELKDEYKGNHCVCKAGHFONTSSPSARCPHTRCENQGLVEAAPGTASDTT 178
DB 161 VLOQPGTEAEVDEIMDIDVNCVPCCKGHPONTSSPSARCPHTRCENQGLVEAAPGTASY 220
QY 179 SDTCKNPPEP 189
DB 221 SDTCKNPPEP 231

RESULT 15
US-09-826-212-6
Sequence 6, Application US/09826212

Patient No. US20010021516A1
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fei
APPLICANT: Gentz, Reiner
APPLICANT: Ruben, Steven
APPLICANT: Ni, Jian
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488,1280006
CURRENT APPLICATION NUMBER: US/09/826,212
CURRENT FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-212-6

Query Match 68.0%; Score 771; DB 9; Length 415;
Best Local Similarity 70.7%; Pred. No. 1.2e-57;
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;

QY 1 SQPQAVPPYASENQTCRDQEKYEYEPQHRICCSRCPPGTIVYSAKCSRIIDTVCATCAENS 60
DB 28 SQPQAVPPYRIENQTCWQDQKEYEYEPMDVCCSCPPGEFVAVCSRSQDITVCKTCPHNS 87
QY 61 YNEHMNYLTICQLCRPCDPVWGIEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSDCP 118
DB 88 YNEHMNYLTICQLCRPCDPVWGIEIAPCTSKRTQCRQCPGMFCAAMALECTHCELLSDCP 147
QY 119 SDCCPTEAEELKDEYKGNHCVCKAGHFONTSSPSARCPHTRCENQGLVEAAPGTASDTT 178
DB 148 VLOQPGTEAEVDEIMDIDVNCVPCCKGHPONTSSPSARCPHTRCENQGLVEAAPGTASY 207
QY 179 SDTCKNPPEP 189
DB 208 SDTCKNPPEP 218

Search completed: August 27, 2004, 21:22:08
Job time : 127 secs

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OM protein - protein search, using sw model

Run on: August 27, 2004, 21:03:31 ; Search time 40 Seconds

(without alignments)
473.743 Million cell updates/sec

Title: US-09-626-219-1

Perfect score: 1133

Sequence: 1 SQQAVPPYASSENQTRDQF.....QSDTTCKNPLEPLPEMMSGT 197

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1133	100.0	435	2	I54182	tumor necrosis fac
2	305	26.9	461	1	A35356	tumor necrosis fac
3	295	26.0	474	2	B38634	tumor necrosis fac
4	290	25.6	459	2	I48854	gene murine tumoun
5	278	24.5	277	2	A60771	B-cell activation
6	243.5	21.5	305	2	A46476	B cell-associated
7	226.5	20.0	651	2	UC7705	death receptor-6 -
8	222.5	19.6	271	2	S12783	OX40 antigen precu
9	214.5	18.9	272	2	I48700	gene oxa4 protein
10	210.5	18.6	455	1	GQHTU1	tumor necrosis fac
11	210	18.5	348	2	T28623	hypothetical protei
12	210	18.5	349	2	D36858	gene G4R protein -
13	207	18.3	349	2	D72175	G2R protein - vari
14	206	18.2	461	2	UC4302	tumor necrosis fac
15	201	17.7	277	2	I37552	OX40 homolog - hum
16	201	17.7	454	1	GOMST1	tumor necrosis fac
17	196	17.3	555	2	A42086	CD30 antigen precu
18	195.5	17.3	255	2	I38426	lymphocyte activat
19	189	16.7	325	2	B43692	t2 protein - rabb
20	187.5	16.5	314	2	I37383	FAS soluble protei
21	184.5	16.3	461	1	GQRTT1	tumor necrosis fac
22	183.5	16.2	336	1	GQVZML	T2 protein - myxom
23	181	16.0	335	2	A40036	apoptosis-mediatin
24	179.5	15.8	256	2	B32393	T-cell antigen 4-1
25	171.5	15.1	425	1	A26431	nerve growth facto
26	166	14.7	435	2	UC5486	membrane glycoprote
27	164	14.5	416	1	JN0006	nerve growth facto
28	162	14.3	327	2	A46484	apoptosis-mediatin
29	148.5	13.1	427	1	GQHNH	nerve growth facto

30	145.5	12.8	324	2	JC2395	Eas antigen precur
31	133	11.7	260	1	A46517	CD27 antigen precu
32	132.5	11.7	1111	2	T26972	hypothetical prote
33	129.5	11.4	1620	2	T27283	hypothetical prote
34	129	11.4	3084	1	MMMSA	laminin alpha-1 ch
35	128.5	11.3	1299	2	T43251	furin (EC 3.4.21.7
36	128	11.3	1274	2	T42017	cysteine rich prot
37	126	11.1	3635	2	T10053	laminin alpha 5 ch
38	125.5	11.1	2180	2	T29764	hypothetical prote
39	124.5	11.0	899	2	G02428	subtilisin-like pr
40	124.5	11.0	915	2	JC6148	subtilisin-like pr
41	124.5	11.0	3707	2	S18252	heparan sulfate pr
42	124	10.9	1680	2	A43434	furin (EC 3.4.21.7
43	123.5	10.9	686	2	JC7569	Delta-4 protein -
44	123	10.9	722	2	I48324	DELTA-like 1 - mou
45	122.5	10.8	915	1	A48225	subtilisin-like pr

ALIGNMENTS

RESULT 1
154182
tumor necrosis factor receptor 2-related protein - human
C/Species: Homo sapiens (man)
C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C/Accession: 154182
R/Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A/Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A/Reference number: 154182; MIM:33252381; PMID:8486360
A/Status: preliminary;
A/Molecule type: mRNA
A/Residues: 1-435 <RES>
A/Cross-references: GB:I04270; NID:9339761; PIRID:AAA36757.1; PID:9339762
C/Genetics:
A/Gene: GDB:LTBR
A/Cross-references: GDB:1230195; OMIM:600979
A/Map position: 12p13.3-12p13.1
C/Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 100.0%; Score 1133; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	SOQAVPPYASENQTRDQFQHRICCSRCPTGVSAKCSIRIDTVCAATCENS	60
DB	28	SOQAVPPYASENQTRDQFQHRICCSRCPTGVSAKCSIRIDTVCAATCENS	87
QY	61	YNHMYVLTICQICRECPVMEIAPCTSKKTCRCOPGMFCAMALECTHCELLSD	120
DB	88	YNHMYVLTICQICRECPVMEIAPCTSKKTCRCOPGMFCAMALECTHCELLSD	147
QY	121	CPPTFAELKDEYGVKNHCVPCKAGHPONTSSPSARCOPHTRCENQGLVEAAPGTASD	180
DB	148	CPPTFAELKDEYGVKNHCVPCKAGHPONTSSPSARCOPHTRCENQGLVEAAPGTASD	207
QY	181	TTCKNPLEPLPEMMSGT	197
DB	208	TTCKNPLEPLPEMMSGT	224

RESULT 2
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N/Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C/Species: Homo sapiens (man)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 27-Oct-2003
C/Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R/Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerez, R.; Dower, S.K.
Science 248, 1019-1023, 1990
A/Title: A receptor for tumor necrosis factor defines an unusual family of cellular and

A:Reference number: A35356; MUID:90260639; PMID:2160731
 A:Accession: A35356
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <SMI>
 A:Cross-references: GB:M2315; NID:q189185; PIDN:AAA59929.1; PID:q189186
 R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
 A:Reference number: A36475; MUID:91045991; PMID:2172983
 A:Accession: A36475
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-195, 'R', 197-461 <KOH>
 A:Cross-references: GB:M55944; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
 R:Denbigh, Z.; Loeschner, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Genetz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
 A:Reference number: A48416; MUID:91370690; PMID:1966549
 A:Accession: A48416
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 23-461 <DEM>
 A:Cross-references: GB:S63368; NID:g235648; PIDN:AA19824.1; PID:g235649
 A:Note: sequence extracted from NCBI backbone (NCBI:M63368, NCBI:M63371).
 R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
 A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
 A:Reference number: A36007; MUID:90349572; PMID:2166946
 A:Accession: A36007
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
 A:Cross-references: GB:M55857; NID:g339751; PIDN:AAA6362.1; PID:g339752
 R:Loeschner, H.; Schlaeger, E.U.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990
 A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
 A:Reference number: A36666; MUID:91056048; PMID:2173696
 A:Accession: A36666
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 23-40; 65-69; 136-141; 300-306 <DOE>
 R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
 A:Reference number: A25010; MUID:90110215; PMID:2153136
 A:Accession: A25010
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-31 <ENG>
 R:Kuhmer, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
 A:Reference number: 138094; MUID:95121934; PMID:7821811
 A:Accession: 138094
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-37 <RES>
 A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
 A:Gene: GDB:TNFR2
 A:Cross-references: GDB:125914; OMIM:191191
 A:Map position: 1p36.2-1p36.2
 A:Introns: 26/3
 A:Note: The list of introns is incomplete
 C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
 F:40-76/Domain: NGF receptor repeat homology <NG1>
 F:78-119/Domain: NGF receptor repeat homology <NG2>
 F:120-162/Domain: NGF receptor repeat homology <NG3>
 F:164-201/Domain: NGF receptor repeat homology <NG4>

F:262-279/Domain: transmembrane #status predicted <TMN>
 F:280-461/Domain: intracellular #status predicted <INT>
 F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 26.0%; Score 305; DB 1; Length 461;
 Best Local Similarity 35.0%; Pred. No. 6, 1e-16;
 Matches 70; Conservative 24; Mismatches 78; Indels 28; Gaps 9;
 5 AVPPYAE NOTGDDQKEYEPEPHRCCSRCPGTYSVAKCSRIPTVCATCAENSYNE 63
 28 AFTPYAPEPSTGCK-LREYVDQAQWCKSGSPGPAKVFCTKTSPTVCDSCEDSTTYQ 85
 64 HMYVLTICQLCR--PCDPVWGLEIAPCTSKRTQCRCPGMFCAMALE-CTHCILLS 119
 86 LMMVPEPCICSGSCSSDY----ETQACTRBEQRITCTCPGWCAUSKQEGGRLCAPLR 141
 120 DCPPG-----TEARLKDEVGKNNHCVPCKAGHPQNTSSPSARCQPHTRCENGLVEAP 174
 142 KCRPGFVAPRGFTSTDVV-----CKPCAPGTFPSNTSTDICRPHQICN----VVAIP 191
 175 GTASDPTTC--KNLEPLP 192
 192 GNASMDVCTSTSTPSMAP 211
 RESULT 3
 B38634
 tumor necrosis factor receptor type 2 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 27-Oct-2003
 C:Accession: B38634; A40254; S54816
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.J. Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r
 A:Reference number: A38634; MUID:91187885; PMID:1849278
 A:Accession: B38634
 A:Molecule type: mRNA
 A:Residues: 1-474 <LEM>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk Mol. Cell. Biol. 11, 3020-3026, 1991
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for t
 A:Reference number: A40254; MUID:91246168; PMID:1645445
 A:Accession: A40254
 A:Molecule type: mRNA
 A:Residues: 1-474 <GOO>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Kisilevsky, M.; Fellous, R.; Felmann, M.; Chernajovsky, Y. submitted to the EMBL Data Library, May 1995
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor.
 A:Reference number: S54816
 A:Accession: S54816
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <KIS>
 A:Cross-references: EMBL:X81128; NID:g809043; PIDN:CAA60618.1; PID:g809044
 C:Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
 C:Keywords: cytokine receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
 F:40-77/Domain: NGF receptor repeat homology <NG1>
 F:79-120/Domain: NGF receptor repeat homology <NG2>
 F:166-203/Domain: NGF receptor repeat homology <NG4>
 Query Match 26.0%; Score 295; DB 2; Length 474;
 Best Local Similarity 34.0%; Pred. No. 3, 5e-15;
 Matches 66; Conservative 24; Mismatches 84; Indels 20; Gaps 8;
 8 PYASE-NQTCRDQKEYEPEPHRCCSRCPGTYSVAKCSRIPTVCATCAENSYNEHN 66
 31 PYKPEPGYECQISQ-EYIDRAQWCCACPCPGQYKHCNCKNSDVTVCADCEASMTQVWN 89
 67 YLTTCOLCR--PCDPVWGLEIAPCTSKRTQCRCPGMFCA--AMALECTHCELLSDC 121

Db 90 QPRTCLSSSSCTTDV---ETIRACTKQONRVACACEGRVCAKTKTHSGSCRCQMRSLKC 145
 QY 122 PEGTEAEIKCEVGNKNNHCVCCKAGHPONTSSPSARCPHTRCENOGIVEAPGTAOSDT 181
 Db 146 GPGF-GVASSRAPNGNVLCKACAPGTFSDTTSSDVCRRPHICS-----ILAIFGNASTDA 200
 QY 182 TCKNPLELPPEMS 195
 Db 201 VC---APESEPTLS 210

RESULT 4

148854 gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)

C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 27-Oct-2003
 C/Accession: 148854
 R/Powell, B.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
 Mamm. Genome 5, 726-727, 1994
 A/Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
 A/Reference number: 148854; MUID:95178848; PMID:7873884
 A/Accession: 148854
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-459 <RES>
 A/Cross-references: EMBL:X/6401; NID:9433830; PIDN:CAA53961.1; PID:9433831
 C/Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology F/151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 25.6%; Score 290; DB 2; Length 459;
 Best Local Similarity 33.5%; Pred. No. 8,2e-15;
 Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;

QY 8 PYASE-NQTRDDEKEYEYEPQHRICSRCPGTYVSAKCSRIRDTVCATCAENSYNHNM 66
 Db 16 PYRPEPEYEQIQG-EYIDKAKQMCCKCPGQYKHFCKTSDTVADCEASMTYQVMN 74
 QY 67 YLITCOLCR--PCDPYMGLEIAPCTSKKTCRCQCPMGFCA--AWALECTHCELLSDC 121
 Db 75 QPRTCLSSSSCTTDV---ETIRACTKQONRVACACEGRVCAKTKTHSGSCRCQMRSLKC 130
 QY 122 PEGTEAEIKCEVGNKNNHCVCCKAGHPONTSSPSARCPHTRCENOGIVEAPGTAOSDT 181
 Db 131 GPGF-GVASSRAPNGNVLCKACAPGTFSDTTSSDVCRRPHICS-----ILAIFGNASTDA 185
 QY 182 TCKNPLELPPEMS 195
 Db 186 VC---APESEPTLS 195

RESULT 5

A60771 B-cell activation protein CD40 precursor - human

N/Alternate names: B-cell surface antigen Bp50
 C/Species: Homo sapiens (man)
 C/Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
 C/Accession: S04460; A60771
 R/Stamenkovic, I.; Clark, E.A.; Seed, B.
 EMBO J. 8, 1403-1410, 1989
 A/Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
 A/Reference number: S04460; MUID:89356608; PMID:2475341
 A/Accession: S04460
 A/Molecule type: mRNA
 A/Residues: 1-277 <STA>
 A/Cross-references: EMBL:X/629850; PIDN:CAA43045.1; PID:929851
 R/Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
 J. Immunol. 142, 562-567, 1989
 A/Title: Biochemical characteristics and partial amino acid sequence of the receptor-11X
 A/Reference number: A60771; MUID:89093941; PMID:2463309
 A/Accession: A60771
 A/Molecule type: protein
 A/Residues: 21-50 <BRA>

A/Experimental source: Burkitt lymphoma cell line Raji
 C/Genetics:
 A/Gene: GDB:CD40
 A/Cross-references: GDB:215268; OMIM:109535
 A/Map position: 20q12-20q13.2
 C/Superfamily: CD27 antigen; NGF receptor repeat homology
 C/Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
 F/1-20/Domain: signal sequence #status predicted <SIG>
 F/21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
 F/21-193/Domain: extracellular #status predicted <EXT>
 F/194-215/Domain: transmembrane #status predicted <TM>
 F/216-277/Domain: intracellular #status predicted <CYT>
 F/153/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.5%; Score 278; DB 2; Length 277;
 Best Local Similarity 35.0%; Pred. No. 4.4e-14;
 Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;

QY 7 PYASENQTRDDEKEYEYEPQHRICSRCPGTYVSAKCSRIRDTVCATCAENSYNHNM 66
 Db 22 PPTA-----CR-EKQYLINSQ--CCSLQPGKLVSDCTEFETETCLPGGSEFDTWN 72
 QY 67 YLITCOLCRCPDPYMGLEIAPCTSKKTCRCQCPMGFCAWALECTHCELLSDCPGTE 126
 Db 73 RETHCHQKXCDDPNTGLRVQCKGTSEDTITCTCEBGNHCSEA--CESCVLHNSCSPFG 130
 QY 127 AEIKCEVGNKNNHCVCCKAGHPONTSSPSARCPHTRCENOGIVEAPGTAOSDTTC 183
 Db 131 VK-QIATGVSDTICECPVGFPSNVSAFCKHPWTSCTETDLVQQAQTNKTDVVC 186

RESULT 6

A46476 B cell-associated surface molecule CD40, long splice form - mouse

C/Species: Mus musculus (house mouse)
 C/Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
 C/Accession: A46476; A46515
 R/Torres, R.M.; Clark, E.A.
 J. Immunol. 148, 620-626, 1992
 A/Title: Differential increase of an alternatively polyadenylated mRNA species of murine
 A/Reference number: A46476; MUID:92105763; PMID:1370315
 A/Accession: A46476
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-305 <TOR>
 A/Cross-references: GB:M83112; NID:91553058
 A/Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)
 A/Note: this translation is not annotated in GenBank entry M83CD40A, release 113.0
 R/Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J.
 J. Immunol. 149, 3921-3926, 1992
 A/Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
 A/Reference number: A46515; MUID:93094586; PMID:1281194
 A/Accession: A46515
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 1-287, 'IV' <GRI>
 A/Cross-references: GB:M83312; NID:91553058; PIDN:AAB08705.1; PID:91553059; GB:M94126; N
 A/Experimental source: BALB/c, liver
 A/Note: sequence extracted from NCBI backbone (NCBI:P:120357)
 C/Comment: For an alternative splice form, see PIR:A46515.
 C/Comment: For an alternative splice form, see PIR:A46476.
 C/Superfamily: CD27 antigen; NGF receptor repeat homology
 C/Keywords: alternative splicing; transmembrane protein
 F/105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 21.5%; Score 243.5; DB 2; Length 305;
 Best Local Similarity 31.0%; Pred. No. 1.9e-11;
 Matches 54; Conservative 22; Mismatches 81; Indels 17; Gaps 5;
 QY 15 TCRDDEKEYEYEPQHRICSRCPGTYVSAKCSRIRDTVCATCAENSYNHNMVLTTCQLC 74
 Db 25 TCSQ--KQYLHDQO--CDLQCPGSRLTSHCTALEKTQCPDCCSGEFSQNMNEIRCHOH 80

[illegible]

RESULT 7
JC7705 death receptor-6 - chicken
C/Species: Gallus gallus (chicken)
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 07-Jul-2003
C/Accession: JC7705
R/Bridgman, J. T.; Bobe, J.; Goetz, F. W.; Johnson, A. L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A/Title: Conservation of death receptor-6 in avian and piscine vertebrates.
C/Reference number: JC7705; PMID:21308433; PMID:11914658

Query March	20.0 %	Score 226.5	DB 2	length 651
Best Local Similarity	28.8 %	Pred. No. 6.5e-10		
Matches 49, Conservative	26	Mismatches 62	Indels 33	Gaps 6

Qy	137	NNHCVPEKAGHFONTSSPSARCOEHTRCENOGUVEAARPGTOSDPTTCKNP	186
Qy	150	DVRCKPLRGTFSDVSSVMKCKTYTDCFGKNMVAVKPGTIESSDNYCXP	199
Db			

RESULT 8
S12783
OX40 antigen precursor - rat
M.Alternate names: nerve growth factor receptor homolog
C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 05-Nov-1999
C.Accession: S12783; S080036
R.Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A.Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte
A.Reference number: S12783; MUID:90214614; PMID:2157591
A.Accession: S12783
A.Molecule type: mRNA
A.Residues: 1-271 <MAL>
A.Cross-references: EXML:X17037; NID:957830; PIDN:CAA34897.1; PID:957831
C.Superfamily: CD27 antigen; NGF receptor repeat homology
C.Keywords: growth factor receptor, transmembrane protein
F1-1/Domain: signal sequence #status predicted <Sig>
F1-20-271/Product: OX40 antigen #status predicted <TM>
F:211-233/Domain: transmembrane #status predicted <TM>

Query Match	19.6%;	Score 222.5;	DB 2;	Length 271;
Best Local Similarity	32.1%;	Pred. No. 6,7e-10;		
Matches	53;	Conservative 17;	Mismatches 68;	Indels 27; Gaps 5

QY	21	KEYEYEHRIICCSRCPGTIVSAKCSIRIDTVCATCAENSYNHEHNYLTICQLCPDCDEY	80
		:::	
Db	28	KDTPPSGHK--CGRCCQGHGMSRCDTRIDTVCHPCEGFYNAEANYDT--CKQCTQCCNHR	85
QY	81	MGLEELAPCTSKRTQCRQCGPMFCAMALECTHCELLSDCPGTGAEALKQEVGKGNHC	140
		:::	
Db	86	SGSELKONCTPTEDETVCCCR-----PGTQPR-QDSHKLGYDC	122
QY	141	VPCEAGHPQNTSSPSARCQPHTRCENOGVLEAPGTAOSDTTCNK	185
Db	123	VPCEPGHSPGSNOA--CKPWTNCTLSKQIRHAPSNSLDVTYCED	165

RESULT 9
I48700
gene ox40 protein - mouse
N:Alternate names: Ox40 antigen
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: I48700; I48334; S34377
R:Calderhead, D.M.; Buhlmann, J.E.; van den Berteigh, A.J.; Claassen, E.; Noelle, R.J.; F
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int
#:Reference number: I48700; MUID:940404750; PMID:82288223

C; Superfamily: CD27 antigen; NGF receptor repeat homology

QY 81 MGLEIAPCTSKRKTRCQCQPMFCALWALEBCTHCELLSDCPGTFABVILKDEVGKANNHC 140
 :::|:::
DB 87 SGSEELKQNTCTPTDTCRCR-----PQTQR-QDSGYKLGVDC 123

QY 141 VPCKAGHFQNTSSP--SARCOPTHRENOGLVEAAPGTAQSTPTCKN 185
124 VPCPFHF----SPGNNOACKFWNTCTLSGKOTRHPASDSLDVAVCED 166
Db

RESULT 10
G0HUT1
tumor necrosis factor receptor 1 precursor [validated] - human
M:alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1
M:contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
C:species: Homo sapiens (man)
C:date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_revision 08-Dec-2000
C:updates: A38208; A34900; A36555; A36581; S12057; U70758; A60231; A33
C:accession: A38208; A34900; A36555; A36581; S12057; U70758; A60231; A33
R:authors: P.; Strahl, S.; Dworzak, M.; Himmelfar, A.; Ambros, F.F.

Genomics 13, 219-224, 1992
 A>Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to ch
 A:Reference number: A38208; MUID:92250049; PMID:1315717
 A:Accession: A38208
 A:Molecule type: DNA
 A:Residues: 1-455 <FUC>
 A:Cross-references: GB:M5864; GB:M75865; GB:M75866; MUID:9339748; PIND:AAA61201.1; PID:9
 R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tüschli, H.; Lessl
 Cell 61, 351-359, 1990
 A>Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep
 A:Reference number: A34899; MUID:90235284; PMID:2158862
 A:Accession: A34899
 A:Molecule type: mRNA
 A:Residues: 1-455 <LOE>
 A:Cross-references: GB:M58286; GB:M33480; MUID:9339753; PIND:AAA36753.1; PID:9339754
 A:Experimental source: Placenta
 A>Note: part of this sequence, including the amino end of the mature protein, confirmed
 Cell 61, 361-370, 1990
 A>Title: Molecular cloning and expression of a receptor for human tumor necrosis factor
 A:Reference number: A34900; MUID:90235285; PMID:2158863
 A:Accession: A34900
 A:Molecule type: mRNA
 A:Residues: 1-455 <SCH>
 A:Cross-references: GB:M33294; MUID:9339744; PIND:AAA03210.1; PID:9339745
 R:Himmeler, A.; Maurer-Fogy, I.; Kroecke, M.; Scheurich, P.; Pfefferle, K.; Lantz, M.;
 DNA Cell Biol. 9, 705-715, 1990
 A>Title: Molecular cloning and expression of human and rat tumor necrosis factor recept
 A:Reference number: A36555; MUID:91090841; PMID:1702293
 A:Accession: A36555
 A:Molecule type: mRNA
 A:Residues: 1-455 <HIM>
 A:Cross-references: GB:M63121; MUID:9339755; PIND:AAA36754.1; PID:9339756
 A:Accession: C36555
 A:Molecule type: protein
 A:Residues: 30-38/41-53, 'X', 55-79, 'XX', 82-94, 'NK', 'XX', 100-104/107-128/162-167, 'X', 169-2
 A>Note: the purified protein, called tumor necrosis factor binding protein, is a soluble
 R:Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
 A>Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re
 A:Reference number: A38281; MUID:91017509; PMID:2170974
 A:Accession: A38281
 A:Molecule type: mRNA
 A:Residues: 1-455 <GRA>
 A:Cross-references: GB:M37764
 A>Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
 R:Nopnar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwarg, R.; Aderka, D.; Holtmann
 EMBO J. 9, 3269-3278, 1990
 A>Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the TNF
 le form of the receptor.
 A:Reference number: S12057; MUID:91006021; PMID:1698610
 A:Accession: S12057
 A:Molecule type: mRNA
 A:Residues: 1-455 <NOP>
 A:Cross-references: EMBL:X55313; MUID:937223; PIND:CA339021.1; PID:937224
 A>Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w
 R:Kemper, O.; Mollach, D.
 Gene 134, 209-216, 1993
 A>Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
 A:Reference number: J70758; MUID:94085779; PMID:8262379
 A:Accession: J70758
 A:Molecule type: DNA
 A:Residues: 1-13 <KEM>
 R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
 Eur. J. Immunol. 20, 1167-1174, 1990
 A>Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
 A:Reference number: A60231; MUID:90292116; PMID:2113477
 A:Accession: A60231
 A:Molecule type: protein
 A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
 R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Incci III, J.A.; Jeffes, E.W.B.; Le
 Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
 A>Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto

tents.
 A:Reference number: A38258; MUID:91062364; PMID:2174164
 A:Accession: A38258
 A:Molecule type: protein
 A:Residues: 41-60 <GAT>
 A:Experimental source: Cancer patient serum
 R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyseil, H.; Grubb, A.; Adolf, G.
 Eur. J. Haematol. 42, 270-275, 1989
 A>Title: Isolation and characterization of a tumor necrosis factor binding protein from
 A:Reference number: A60594; MUID:89171156; PMID:2924890
 A:Accession: A60594
 A:Molecule type: protein
 A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XX', 60 <OLS>
 A:Experimental source: renal failure patient urine
 R:Engelmann, H.; Novick, D.; Wallach, D.
 J. Biol. Chem. 265, 1531-1536, 1990
 A>Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
 A:Reference number: A35010; MUID:90110215; PMID:2153136
 A:Accession: A35010
 A:Molecule type: protein
 A:Residues: 41-45 <ENG>
 A:Experimental source: normal urine
 R:Kajihara, J.; Asada, A.; Kirihaara, S.; Kato, K.
 Biochem. Biotechnol. Blochem. 58, 2266-2268, 1994
 A>Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f
 A:Reference number: JC2404; MUID:95128033; PMID:7765720
 A:Accession: JC2404
 A:Molecule type: protein
 A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>
 A:Experimental source: urine
 C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
 C:Gene: GDB:TNFR1
 A:Gene: GDB:TNFR1
 A:Cross-references: GDB:125913; OMIM:191190
 A:Map position: 12p13.2-12p13.2
 A:Intons: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-45/Domain: signal sequence #status predicted <SIG>
 F:46-211/Domain: extracellular #status predicted <EXT>
 F:41-201/Domain: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
 F:44-82/Domain: NGF receptor repeat homology <NG1>
 F:84-126/Domain: NGF receptor repeat homology <NG2>
 F:127-167/Domain: NGF receptor repeat homology <NG3>
 F:168-196/Domain: NGF receptor repeat homology <NG4>
 F:212-234/Domain: transmembrane #status predicted <MEM>
 F:235-455/Domain: intracellular #status predicted <INT>
 F:54/145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.6%; Score 210.5; DB 1; Length 455;
 Best Local Similarity 32.6%; Pred. No. 8e-09;
 Matches 61; Conservative 19; Mismatches 84; Indels 23; Gaps 9;

QY	18	DOEK-----EYEPQHR-ICSRCPGTYSAKC-SRIRDVATCAENSYNHHWY	67
DB	36	DEKRDVCPQGXKYIHPQNNISICTKHKHGTLYNDCCPPQDDTCREBSGSFTASENH	95
QY	68	LTICQLCPDCPDVMEGLBAPTSKRTQRCQCPGFCAMAA--LECHCELLSDCPG	124
DB	96	LRHCSGSKCRKEMQVEISSCTVDRDVCGRKQYRHYWSENLFOCFNCST--CLNG	152
QY	125	TEAFLKDEYGVKNNHCVCKAGH--ONTSSSARCPHTRENGCL--VEAAPTGAQSD	180
DB	153	TVHLSQGF--KONTVCT--CHAGFLREBVCVSCNCKSLCTKLCTLQIENVKGTEDSG	209
QY	181	TTCKNPL 187	
DB	210	TTVLLPL 216	

RESULT 11
 128623

Hypothetical protein G2R - variola major virus

C/Species: variola major virus

C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Sep-2003

C/Accession: T28623

R/Masung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utechtack, T.R.; Knight, J.C.; Aubin

Nature 366, 748-751, 1993

A/Title: Potential virulence determinants in terminal regions of variola smallpox virus

A/Reference number: Z20488; MUID:94088747; PMID:8264798

A/Accession: T28623

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1348 <AMS>

A/Cross-references: EMBL:L22579; NID:G623595; PIDN:AAA60933.1; PID:G439102

A/Experimental source: strain Bangladesh 1975

C/Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

Query Match 18.5%; Score 210; DB 2; Length 348;

Best Local Similarity 29.0%; Pred. No. 7.1e-09; Mismatches 80; Indels 10; Gaps 5;

Matches 45; Conservative 20; Mismatches 80; Indels 10; Gaps 5;

QY 8 PYASENOTCRDOEKEYEYEPQHRICSRCPGTYVSACSKSRIRDTVCATCAENSYNEHMY 67

Db 23 PYTPPNKCKDTEYK----RHNLCCLSCPRTYASRLCDSKTNQCTPCGSGFTSRNNH 78

QY 68 LTTICQLCR-PCDPVWGLBEIAPCTSKRTQCRQCPGMFC-AAAALFCHCEILSDCPPT 125

Db 79 LPACLSGNGRCN--SNQVETRSCNTTNHRIECSPGYCLKSGGCKACVSTKTC--GI 134

QY 126 EAEIKDEVGKGNHCVPCCKAGHPONTSSPSARCP 160

Db 135 GYGVSGHTSVGDVICSFGRTYSHYSSADKCEP 169

RESULT 12

D36858

gene G4R protein - variola virus

N/Alternate names: B2ER protein (COP)

C/Species: variola virus

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Sep-2003

C/Accession: D36858; S46888; S33385; S35987

R:Blinov, V.M.

submitted to GenBank, November 1992

A/Reference number: A36859

A/Accession: D36858

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-349 <BHI>

A/Cross-references: GB:X69198; NID:G456758; PIDN:CAA49137.1; PID:G457087

A/Experimental source: strain India-1967, ssp. major, isolate Ind3

R:Kolymhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chiznikov, V.E.; Frolov

submitted to the EMBL Data Library, April 1992

A/Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P

A/Reference number: S46868

A/Accession: S46868

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-349 <KOL>

A/Cross-references: EMBL:X67117; NID:G516428; PIDN:CAA47540.1; PID:G516449

A/Experimental source: strain India-1967, isolate Ind3

R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.

FEBS Lett. 319, 80-83, 1993

A/Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

A/Reference number: S33385; MUID:93202281; PMID:8584129

A/Accession: S33385

A/Molecule type: DNA

A/Residues: 31-168 <SHC>

A/Cross-references: EMBL:X69198

A/Experimental source: strain India-1967, ssp. major

C/Genetics:

A/Gene: G4R

C/Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

F:32-66/Domain: NGF receptor repeat homology <NGF>

F:68-109/Domain: NGF receptor repeat homology <NG2>

F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 18.5%; Score 210; DB 2; Length 349;

Best Local Similarity 29.0%; Pred. No. 7.1e-09; Mismatches 80; Indels 10; Gaps 5;

Matches 45; Conservative 20; Mismatches 80; Indels 10; Gaps 5;

QY 8 PYASENOTCRDOEKEYEYEPQHRICSRCPGTYVSACSKSRIRDTVCATCAENSYNEHMY 67

Db 24 PYTPPNKCKDTEYK----RHNLCCLSCPRTYASRLCDSKTNQCTPCGSGFTSRNNH 79

QY 68 LTTICQLCR-PCDPVWGLBEIAPCTSKRTQCRQCPGMFC-AAAALFCHCEILSDCPPT 125

Db 80 LPACLSGNGRCN--SNQVETRSCNTTNHRIECSPGYCLKSGGCKACVSTKTC--GI 135

QY 126 EAEIKDEVGKGNHCVPCCKAGHPONTSSPSARCP 160

Db 136 GYGVSGHTSVGDVICSFGRTYSHYSSADKCEP 170

RESULT 13

D72175

G2R protein - variola minor virus (strain Garcia-1966)

C/Species: variola minor virus

C/Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 15-Sep-2003

C/Accession: D72175

R:Shchelkunov, S.N.; Tchemin, A.V.; Gutorov, V.V.; Safonov, P.F.; Masung, R.F.; Lopate

submitted to GenBank, March 1998

A/Description: Analysis of the complete coding sequence of DNA of alastrim variola minor

A/Reference number: A72150

A/Accession: D72175

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-349 <SHC>

A/Cross-references: GB:Y16780; NID:G5830555; PIDN:CAB54798.1; PID:G5830759

A/Experimental source: strain Garcia-1966

C/Genetics:

A/Gene: G2R

C/Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

Query Match 18.3%; Score 207; DB 2; Length 349;

Best Local Similarity 29.0%; Pred. No. 1.2e-08; Mismatches 81; Indels 10; Gaps 5;

Matches 45; Conservative 19; Mismatches 81; Indels 10; Gaps 5;

QY 8 PYASENOTCRDOEKEYEYEPQHRICSRCPGTYVSACSKSRIRDTVCATCAENSYNEHMY 67

Db 24 PYTPPNKCKDTEYK----RHNLCCLSCPRTYASRLCDSKTNQCTPCGSGFTSRNNH 79

QY 68 LTTICQLCR-PCDPVWGLBEIAPCTSKRTQCRQCPGMFC-AAAALFCHCEILSDCPPT 125

Db 80 LPACLSGNGRCN--SNQVETRSCNTTNHRIECSPGYCLKSGGCKACVSTKTC--GI 135

QY 126 EAEIKDEVGKGNHCVPCCKAGHPONTSSPSARCP 160

Db 136 GYGVSGHTSVGDVICSFGRTYSHYSSADKCEP 170

RESULT 14

JC4302

tumor necrosis factor receptor p55 precursor - pig

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999

C/Accession: JC4302; PC4093

R:Suter, B.; Pauli, U.

Gene 163, 263-266, 1995

A/Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.

A/Reference number: JC4302; MUID:96011645; PMID:7590278

A/Accession: JC4302

A/Molecule type: mRNA

A/Residues: 1-461 <SUT>

A/Cross-references: GB:U19994; NID:G141752; PIDN:AAC48499.1; PID:G141753

A/Experimental source: strain India-1967, ssp. major

C/Genetics:

A/Gene: G4R

C/Superfamily: TNF-alpha receptor-II; NGF receptor repeat homology

F:32-66/Domain: NGF receptor repeat homology <NGF>

F:68-109/Domain: NGF receptor repeat homology <NG2>

A:Experimental source: kidney cell line 15

C:Genetics:

A:Gene: tnfr

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>

F/44-194/Domain: extracellular cysteine rich #status predicted <EXT>

F/44-82/Domain: NGF receptor repeat homology <NGF>

F/84-126/Domain: NGF receptor repeat homology <NGF>

F/211-231/Domain: transmembrane #status predicted <TM>

F/361-447/Domain: signal transduction #status predicted <ST>

F/54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 18.2%; Score 206; DB 2; Length 461;

Matches 57; Conservative 22; Mismatches 73; Indels 38; Gaps 9;

QY 18 DQEK-----EYEPQHR-ICSRCPPTVYSAK-SRIADTVCAICANSYNEHMY 67

Db 36 DREKRESLCPQKSHPNRSICCTCKHGTIYIANDCLGPGLDIDCRDNGTPTASENH 95

QY 68 LITQQLCPDPVWGLEIAPCTSKRTQCRQCPGMCAWA---LECTHCELSDCPPG 124

Db 96 LTQCLSCSKCRSEMSOYEISPTVDRDITVCGCRKNQYKXWSETLFCCLNCSL---CPNG 152

QY 125 TE---AEIKDEVGKNNHCPCAKGHONTSSPASCQPHTRCENOGVEAPGTAO-- 178

Db 153 TVQLPCLBKQDTI-----CNCHSGFPLR---DKECVSCVCKNADCKNLCPATSETR 201

QY 179 ----SDITCKNPL 187

Db 202 NDFQDTGTTLPL 215

RESULT 15

I37552

OX40 homolog - human

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000

C:Accession: I37552

R;Lectza, U.; Durkop, H.; Schnitzler, S.; Ringeling, J.; Ritelbach, F.; Hummel, M.; Fonat

Eur. J. Immunol. 24, 677-683, 1994

A>Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment

A:Reference number: I37552; MUID:94170844; PMID:7510240

A:Accession: I37552

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-277 <RES>

A:Cross-references: EMBL:X75962; NID:9472957; PID:CA53576.1; PID:9472958

C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match

Best Local Similarity 17.7%; Score 201; DB 2; Length 277;

Matches 49; Conservative 21; Mismatches 73; Indels 30; Gaps 5;

QY 26 POHRICSRPPPTVYSAKSRITDYCATCAENSYNEHMYLTICQLCPDPVWGLEE 85

Db 37 PSNDRCCHRCRPNQWRSRSQNTVCRPGGFYNDVVSXP-CXPTWCMLRSGER 95

QY 86 IAPCTSKRTQCRQCPGMCAWALBCTHCELSDCPGEARLKDVGKNNHCVPCKA 145

Db 96 KQICTATQDTVCCKRAG-----TQPLDSTYKPGVD-----CAPCP 130

QY 146 GHFQNTSSPASCQPHTRCENOGVEAPGTASDTTC--KNPLEPLPPMSG 196

Db 131 GHF--SPGDNQACKPWTNCTLAGKHTLQPASNSDAICEDRDPAPATQPOETG 181

Search completed: August 27, 2004, 21:11:09

Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 27, 2004, 20:54:45 ; Search time 128 Seconds

(without alignments)
434.858 Million cell updates/sec

Title: US-09-626-219-1

1133

Sequence: 1 SQPAPVPPYSENQTCRDE.....QSDTCKNPDEPPENSGT 197

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1133	100.0	197	2	AAW32220 Extracellular
2	1133	100.0	197	2	AAW31326 Human lym
3	1133	100.0	435	6	ABP96137 Human TNF
4	1133	100.0	435	6	ABR40220 Human gen
5	1133	100.0	435	6	ABU89821 TNF-recep
6	1129	99.6	399	6	ABP96136 Human TNF
7	1108	97.8	416	7	ADCA2856 Human TNF
8	987	87.1	170	6	ADA49700 Extracell
9	771	68.0	415	4	ABP36700 Human tum
10	771	68.0	415	6	ABP96138 Human lym
11	456	40.2	77	4	AAW94642 TNF-R ext
12	456	40.2	77	4	AAW94642 TNF-R ext
13	381.5	33.7	305	5	ABP41926 Human TNF
14	315	27.8	518	2	AAW59665 Human sol
15	311.5	27.5	659	6	ABU57103 Concatame
16	309	27.3	461	2	AAW72504 p75 Tumou
17	307	27.1	720	6	ABJ37101 Concatame
18	305	26.9	225	6	AAW77463 Primate p
19	305	26.9	227	4	AAW69691 Human tum
20	305	26.9	235	2	AAW59665 Human sol
21	305	26.9	235	2	AAW52270 Tumour ne
22	305	26.9	235	2	AAW52270 Tumour ne
23	305	26.9	235	2	AAW52270 Tumour ne
24	305	26.9	235	2	AAW52270 Tumour ne
25	305	26.9	235	2	AAW52270 Tumour ne

26	305	26.9	235	4	AAW37685	AAW37685 Human 40
27	305	26.9	235	6	ADA20593	ADA20593 Human 40k
28	305	26.9	248	3	AAW94718	AAW94718 Human typ
29	305	26.9	355	6	ADA09891	ADA09891 Human rec
30	305	26.9	461	2	AAW11141	AAW11141 Human TNF
31	305	26.9	461	2	AAW11001	AAW11001 40kD TNF
32	305	26.9	461	2	AAW42058	AAW42058 Fibroblas
33	305	26.9	461	3	AAW01342	AAW01342 Death rec
34	305	26.9	461	3	AAW18717	AAW18717 A human t
35	305	26.9	461	4	AAW37801	AAW37801 Human tum
36	305	26.9	461	4	AAW35331	AAW35331 Human TNF
37	305	26.9	461	4	AAW37686	AAW37686 Human 40
38	305	26.9	461	4	AAW36698	AAW36698 Human tum
39	305	26.9	461	5	AAW75172	AAW75172 Human TNF
40	305	26.9	461	5	AAW75173	AAW75173 Human TNF
41	305	26.9	461	5	AAW75173	AAW75173 Human TNF
42	305	26.9	461	5	ABP52451	ABP52451 Human tum
43	305	26.9	461	6	ABR55854	ABR55854 Human tum
44	305	26.9	461	6	ABR39799	ABR39799 Human DIS
45	305	26.9	461	6	ABO53256	ABO53256 Human tum

ALIGNMENTS

RESULT 1
AAW32220
ID AAW32220 standard; protein; 197 AA.

AAW32220;

29-OCT-1997 (first entry)

Extracellular domain of human lymphotoxin beta receptor.

Human; lymphotoxin beta; receptor; blocking agent; extracellular;
ligand binding; domain; treatment; Th1 cell; immune response; delayed;
hypersensitivity; contact; tuberculin; granulomatous; graft versus host;
disease; organ rejection; autoimmune; disorder; multiple sclerosis;
insulin dependent diabetes; uveitis; cytokine; sympathetic ophthalmia;
psoriasis; diceritis; Toxoplasma; infection; Mycobacterium; abnormal;
lymphoid organ; development.

OS Homo sapiens.

PN WO9703687-A1.

PD 06-FEB-1997.

PF 19-JUL-1996; 96WO-US012010.

PR 21-JUL-1995; 95US-00505606.

PA (BIOT) BIOGEN INC.

PI Browning JL, Benjamin CD, Hochman PS,

WPI; 1997-132373/12.

Compositions comprising lymphotoxin-beta receptor blocking agent - used
to treat autoimmune diseases, e.g. sclerosis, insulin-dependent
diabetes, etc.

Example 1; Page 55-56; 76pp; English.

The present sequence, a human lymphotoxin beta receptor (LT-beta-R)
blocking agent, comprises the extracellular ligand binding domain of the
human LT-beta-R up to the transmembrane region. It can be used to treat a
Th1 cell mediated immune response which contributes to a delayed type
hypersensitivity reaction, preferably contact, tuberculin type or
granulomatous hypersensitivity, graft versus host disease, organ
rejection or an autoimmune disorder, i.e. multiple sclerosis, insulin
dependent diabetes, sympathetic ophthalmia, uveitis and psoriasis. It can

CC also be used to treat conditions exacerbated by the activities of Th-1
CC type cytokines, or listeria, toxoplasma or Mycobacterium infection. Its
CC ability to selectively or partially block the LT-beta-R pathway may be
CC useful in the treatment of abnormal lymphoid organ development associated
CC with misexpression or overexpression of signalling by the LT-beta-R
CC pathway. The present LT-beta-R blocking agent is capable of selectively
CC inhibiting Th1, but not Th2 cell dependent immune effector mechanisms. As
CC Th1 cytokines can inhibit Th2 cell dependent responses, the present LT-
CC beta-R blocking agent may also indirectly stimulate certain Th2 cell
CC dependent responses which are normally inhibited by Th1 induced
CC cytokines. Doses of about 1 mg/kg of the present soluble LT-beta-R are
CC expected to be suitable starting doses for optimising treatment

XX Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPVASENQTCDQDEKEYEPQHRICCSRCPRGTYSACSRIRDTVCATCENS 60
DB 1 SQPQAVPPVASENQTCDQDEKEYEPQHRICCSRCPRGTYSACSRIRDTVCATCENS 60
QY YNEHWNVLTITCOLCRPCDPVWGLEBIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
DB YNEHWNVLTITCOLCRPCDPVWGLEBIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
QY 121 CPPTGEALDKDEVGKGNHCVCKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTASD 180
DB 121 CPPTGEALDKDEVGKGNHCVCKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTASD 180
QY 181 TTCNKLPLEPLPEMSGT 197
DB 181 TTCNKLPLEPLPEMSGT 197

RESULT 2

AAV31326

ID AAV31326 standard; peptide; 197 AA.

AAV31326;

DT 04-OCT-1999 (first entry)

Human lymphotoxin (LT) beta-receptor extracellular region.
Lymphotoxin-beta; LT-beta; LT-beta receptor; follicular dendritic cell;
immune system; tumour; follicular lymphoma; extracellular domain; human.

Homo sapiens.

WO938525-A1.

05-AUG-1999.

29-JAN-1999; 99WO-US001928.

30-JAN-1998; 98US-0073112P.

02-FEB-1998; 98US-0073410P.

(BIOJ) BIOGEN INC.

Browning J, Thorbecke J, Tsiasge V;

WPI; 1999-469242/39.

New method of treating follicular lymphomas by inhibiting interaction
between lymphotoxin-beta and its receptor.

Example 1; Page 25-26; 31pp; English.

The invention provides a method for arresting or reducing, severity of
effects of a tumour by administration of a composition which inhibits the

CC interaction between lymphotoxin (LT) beta and its receptor. An inhibitor
CC of the interaction between LT-beta and its receptor can be administered
CC for altering the survival or maintenance of follicular dendritic cells in
CC a subject and for altering the architecture of the organs of the immune
CC system. The method is useful for treating tumours, specifically
CC follicular lymphomas. It offers an alternative therapy for those with
CC tumours resistant to traditional chemotherapy. The present sequence
CC comprises the ligand binding domain

XX Sequence 197 AA;

Query Match 100.0%; Score 1133; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPPVASENQTCDQDEKEYEPQHRICCSRCPRGTYSACSRIRDTVCATCENS 60
DB 1 SQPQAVPPVASENQTCDQDEKEYEPQHRICCSRCPRGTYSACSRIRDTVCATCENS 60
QY YNEHWNVLTITCOLCRPCDPVWGLEBIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
DB YNEHWNVLTITCOLCRPCDPVWGLEBIAPCTSKRTQCRQCPGMFCAMALECTHCELLSD 120
QY 121 CPPTGEALDKDEVGKGNHCVCKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTASD 180
DB 121 CPPTGEALDKDEVGKGNHCVCKAGHFQNTSSPSARCQPHTRCENOGIVEAPGTASD 180
QY 181 TTCNKLPLEPLPEMSGT 197
DB 181 TTCNKLPLEPLPEMSGT 197

RESULT 3

ABP96137

ID ABP96137 standard; protein; 435 AA.

ABP96137;

DT 09-MAY-2003 (first entry)

Human TNF receptor 2 related protein/LTRbeta SHQ ID NO:19.
Human; tumour necrosis factor receptor 2 related protein variant;
TNFR2PV; cytostatic; immunosuppressive; antiasthmatic; gene therapy;
TNF signalling; cancer; inflammatory disorder; rheumatoid arthritis;
asthma; ulcerative colitis.

Homo sapiens.

WO2003012037-A2.

13-FEB-2003.

24-JUL-2002; 2002WO-US023684.

27-JUL-2001; 2001US-00917372.

(INCY-) INCYTE GENOMICS INC.

Lal PG, Warren BA;

WPI; 2003-256445/25.

New cDNA, useful for preparing a composition for treating a disease or
condition associated with increased TNF signaling e.g., cancer of the
prostate, ovary, gallbladder, breast, brain, liver or colon, or
rheumatoid arthritis, asthma.

Disclosure; Fig 2A-C; 64pp; English.

The present invention describes human tumour necrosis factor receptor 2
related protein variant (TNFR2PV). TNFR2PV has cytostatic, antiasthmatic

effects of a tumour by administration of a composition which inhibits the

CC and immunosuppressive activities, and can be used in gene therapy. The
CC TNFR2PV CDNA or protein sequences can be used for preparing a composition
CC for treating a disease or condition associated with increased TNF
CC signalling e.g., cancer of the prostate, ovary, gallbladder, breast,
CC brain, liver or colon, or inflammatory disorders, such as rheumatoid
CC arthritis, asthma or ulcerative colitis. The present sequence represents
CC a human TNFR2 related protein/LTRbeta amino acid sequence, which is given
CC in comparison with human TNFR2PV in the exemplification of the present
CC invention
XX
SQ Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPYASENQTRDQKEYEYEPQHRICSRCPGTYSACSRIRDTVCATCAENS 60
DB 28 SQPQAVPYASENQTRDQKEYEYEPQHRICSRCPGTYSACSRIRDTVCATCAENS 87
QY 61 YNEHMYVLTICQLCRPCDPVWGIEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 120
DB 88 YNEHMYVLTICQLCRPCDPVWGIEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 147
QY 121 CPFGTEAEIKDEVGKGNHCVCKAGHFONTSSPSARCOPTHRCENQGLVEAARGTAQSD 180
DB 148 CPFGTEAEIKDEVGKGNHCVCKAGHFONTSSPSARCOPTHRCENQGLVEAARGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224

RESULT 4
ID ABR40220 standard; protein; 435 AA.

AC ABR40220;

DT 12-JUN-2003 (first entry)

XX Human genoxin.

XX Human; genoxin; antiarteriosclerotic; antidiabetic; hypotensive;
KW antilipemic; anorectic; immunomodulator; cytoskeletal; anti-HIV;
KW antiinflammatory; cardiant; cerebroprotective; gene therapy;
KW tumour necrosis factor receptor; TNFR; body mass; weight loss; obesity.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..30

FT Protein /label= Signal_peptide 31..435

FT Domain /label= Mature_genoxin 31..227

FT Domain /label= Extracellular_domain 228..248

FT Domain /label= Transmembrane_domain 249..435

FT Domain /label= Intracellular_domain

PN WO2003011322-A1.

PD 13-FEB-2003.

PF 31-JUL-2002; 2002WO-IB003417.

PR 02-AUG-2001; 2001US-0309917P.

PA (GENSET) GENSET SA.

XX Lucas J, Dialynas D, Briggs K,

XX WPI; 2003-256417/25.
DR N-PSDB; AB299578.

PT Screening for an agonist or antagonist of Genoxin activity, useful for
PT preventing or treating metabolic disorders, comprises contacting Genoxin
PT polypeptide with a test compound and determining binding.

PS Example 10; Page 33-34; 37pp; English.

XX The invention relates to a novel method for screening for an agonist or
CC antagonist of Genoxin activity. The agonists/antagonists of the invention
CC have antiarteriosclerotic, antidiabetic, hypotensive, antilipemic,
CC anorectic, immunomodulator, cytoskeletal, anti-HIV, antiinflammatory,
CC cardiant, and cerebroprotective activity. The polypeptides of the
CC invention may have a use in gene therapy, and act as tumour necrosis
CC factor receptor (TNFR) agonists. The method is used to screen for an
CC agonist or antagonist of Genoxin. The method is useful in metabolic
CC research, particularly, in discovering compounds that modulate Genoxin
CC activity or that reduce or increase body mass and maintain weight loss,
CC and in preventing or treating obesity-related diseases or disorders such
CC as hyperlipidaemia, atherosclerosis, heart disease, stroke, insulin-
CC resistant diabetes or hypertension, or for preventing or treating
CC disorders associated with excessive weight loss, such as cachexia, cancer
CC weight loss, chronic inflammatory disease-related weight loss, or
CC anorexia. The present sequence represents the human genoxin of the
CC invention
XX

SQ Sequence 435 AA;

Query Match 100.0%; Score 1133; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQPQAVPYASENQTRDQKEYEYEPQHRICSRCPGTYSACSRIRDTVCATCAENS 60
DB 28 SQPQAVPYASENQTRDQKEYEYEPQHRICSRCPGTYSACSRIRDTVCATCAENS 87
QY 61 YNEHMYVLTICQLCRPCDPVWGIEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 120
DB 88 YNEHMYVLTICQLCRPCDPVWGIEIAPCTSKRTQCRQPGMFCAMALECTHCELLSD 147
QY 121 CPFGTEAEIKDEVGKGNHCVCKAGHFONTSSPSARCOPTHRCENQGLVEAARGTAQSD 180
DB 148 CPFGTEAEIKDEVGKGNHCVCKAGHFONTSSPSARCOPTHRCENQGLVEAARGTAQSD 207
QY 181 TTCKNPLEPLPPMSGT 197
DB 208 TTCKNPLEPLPPMSGT 224

RESULT 5
ID ABR89821

XX ABR89821 standard; protein; 435 AA.

AC ABR89821;

DT 10-JUL-2003 (first entry)

XX TNF-receptor associated factor 5 (TRAF5) interacting protein #1.

XX Human; cytoskeletal; DAPK3-Agonist; DAPK3-Antagonist; cancer;

XX TNF-receptor associated factor 5 interacting protein;

XX tumour necrosis factor associated factor 5 interacting protein;

XX TRAF5 interacting protein.

XX Homo sapiens.

PN WO2003031571-A2.

PD 17-APR-2003.

PF 02-OCT-2002; 2002MO-US031357.
XX
XX 05-OCT-2001; 2001US-0327454P.
PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 25-JUN-2002; 2002US-0391342P.
PR 01-OCT-2002; 2002US-00262445.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Burgess CE, Catterton E, Chant JS, Chaudhuri A;
PI Edinger SR, Gerlach VL, Giot L, Gorman L, Guo X, Kekuda R,
PI Mezes PS, Millet I, Ooi CE, Paturajan M, Rieger DK, Spytek KA;
PI Taupier RJ, Zehusen BD, Zhong H, Zhong M;
XX
XX WPI: 2003-381704/36.
DR N-PSDB; ACA90237.
XX
XX New DAPK3 polypeptide, useful for preparing a composition for treating or
PT preventing e.g., cancer.
XX
XX Example 20F; Page 240; 253pp; English.
XX
XX The invention describes an isolated polypeptide comprising any of 33 90-
CC 1273 amino acid sequences (I) given in the specification or its mature
CC form, a sequence that is at least 95 % identical to (I), or a sequence
CC comprising one or more conservative substitutions in the amino acid
CC sequence of (I). The polypeptide is useful for preparing a composition
CC for treating or preventing e.g., cancer. This is the amino acid sequence
CC of a tumor necrosis factor (TNF)-receptor associated factor 5 (TRAF5)
CC interacting protein associated with the identification of novel human
CC proteins and their functions
XX
XX Sequence 435 AA;
SQ
Query Match 100.0%; Score 1133; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.3e-78;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOPQAVPPYASENOTCRDOEKYEYEPORHICCRCPPTGYVSAAKCSRIIDTVCAATCAENS 60
DB 28 SOPQAVPPYASENOTCRDOEKYEYEPORHICCRCPPTGYVSAAKCSRIIDTVCAATCAENS 87
QY 61 YNEHNNVLTICQLCRPCDPVWGLEIAPCTSRKKTQCRQCPGMFCAMALBCTHCELLSD 120
DB 88 YNEHNNVLTICQLCRPCDPVWGLEIAPCTSRKKTQCRQCPGMFCAMALBCTHCELLSD 147
QY 121 CPPGTAEALIKDEVGKGNHCVCKAGHFOHTSSPSARQCPHTRCENOGIVEAAPGTAOSD 180
DB 148 CPPGTAEALIKDEVGKGNHCVCKAGHFOHTSSPSARQCPHTRCENOGIVEAAPGTAOSD 207
QY 181 TTCKNPLELPPEMSGT 197
DB 208 TTCKNPLELPPEMSGT 224
RESULT 6
ABP96136
ID ABP96136 standard; protein; 399 AA.
XX
XX ABP96136;
AC
XX
XX 09-MAY-2003 (first entry)
DT
XX
XX Human TNF receptor 2 related protein variant SEQ ID No.1.

XX
XX Human; tumour necrosis factor receptor 2 related protein variant;
KW TNFR2PV; cytosstatic; immunosuppressive; antiasthmatic; gene therapy;
KW TNF signaling; cancer; inflammatory disorder; rheumatoid arthritis;
KW asthma; ulcerative colitis.
XX
XX Homo sapiens.
XX
XX W02003012037-A2.
XX
XX 13-FEB-2003.
XX
XX 24-JUL-2002; 2002MO-US023684.
XX
XX 27-JUL-2001; 2001US-00917372.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX L1a1 Fg, Warren BA;
PI
XX
XX WPI: 2003-256445/25.
DR N-PSDB; ABZ79717.
XX
XX New CDNA, useful for preparing a composition for treating a disease or
PT condition associated with increased TNF signaling e.g., cancer of the
PT prostate, ovary, gallbladder, breast, brain, liver or colon, or
PT rheumatoid arthritis, asthma.
XX
XX Claim 20; Fig 1A-F; 64pp; English.
XX
XX The present sequence represents human tumour necrosis factor receptor 2
CC related protein variant (TNFR2PV). TNFR2PV has cytosstatic, antiasthmatic
CC and immunosuppressive activities, and can be used in gene therapy. The
CC TNFR2PV cDNA or protein sequences can be used for preparing a composition
CC for treating a disease or condition associated with increased TNF
CC signaling e.g., cancer of the prostate, ovary, gallbladder, breast,
CC brain, liver or colon, or inflammatory disorders, such as rheumatoid
CC arthritis, asthma or ulcerative colitis
XX
XX Sequence 399 AA;
SQ
Query Match 99.6%; Score 1129; DB 6; Length 399;
Best Local Similarity 99.5%; Pred. No. 4.3e-78;
Matches 196; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOPQAVPPYASENOTCRDOEKYEYEPORHICCRCPPTGYVSAAKCSRIIDTVCAATCAENS 60
DB 28 SOPQAVPPYASENOTCRDOEKYEYEPORHICCRCPPTGYVSAAKCSRIIDTVCAATCAENS 87
QY 61 YNEHNNVLTICQLCRPCDPVWGLEIAPCTSRKKTQCRQCPGMFCAMALBCTHCELLSD 120
DB 88 YNEHNNVLTICQLCRPCDPVWGLEIAPCTSRKKTQCRQCPGMFCAMALBCTHCELLSD 147
QY 121 CPPGTAEALIKDEVGKGNHCVCKAGHFOHTSSPSARQCPHTRCENOGIVEAAPGTAOSD 180
DB 148 CPPGTAEALIKDEVGKGNHCVCKAGHFOHTSSPSARQCPHTRCENOGIVEAAPGTAOSD 207
QY 181 TTCKNPLELPPEMSGT 197
DB 208 TTCKNPLELPPEMSGT 224
RESULT 7
ADC42856
ID ADC42856 standard; protein; 416 AA.
XX
XX ADC42856;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX REMAP protein #16.
DE
XX
XX Cytostatic; Antiarteriosclerotic; Anti-HIV; Antiinflammatory;

KM Antiallergic; Antidiabetic; REMAP; pathogenesis.

OS Homo sapiens.

XX WO2003027228-A2.

XX 03-APR-2003.

XX 16-JUL-2002; 2002WO-US022833.

XX 17-JUL-2001; 2001US-0306020P.

XX 27-JUL-2001; 2001US-0308179P.

XX 02-AUG-2001; 2001US-0309702P.

XX 10-AUG-2001; 2001US-0311476P.

XX 10-AUG-2001; 2001US-0311551P.

XX 10-AUG-2001; 2001US-0311718P.

XX 24-AUG-2001; 2001US-0314798P.

XX 31-AUG-2001; 2001US-0316639P.

XX 07-SEP-2001; 2001US-0317996P.

XX (INCY-) INCYTE GENOMICS INC.

XX 1al PG, Honchell CD, Forsythe IU, Walla NK, Tang TY, Borowsky ML;

XX Barroso I, Yue H, Warren BA, Thangavelu K, Gietzen KJ, Azimzai Y;

XX Lee EA, Baughn MR, Corvada AE, Duggan BM, Tran B, Li JY, Azimzai Y;

XX Richardson TW, Elliott VS, Zebajadian Y, Tran UK, Yao MG,

XX Peterson DP, Luo W, Leht-Mason PM;

XX WPI; 2003-421156/39.

XX New human receptors and membrane-associated proteins (REMAP), useful for

XX diagnosing, treating or preventing disorders associated with aberrant

XX REMAP expression, e.g. cancer, AIDS, atherosclerosis, hypertension or

XX stroke.

XX Claim 1; SEQ ID NO 16; 115pp; English.

XX The present invention relates to an isolated polypeptide. The

XX polypeptides and polynucleotides are useful in diagnosing, treating and

XX preventing disorders associated with aberrant expression of REMAP, such

XX as cell proliferative, autoimmune/inflammatory, renal, neurological,

XX cardiovascular, metabolic, developmental, endocrine, muscle,

XX gastrointestinal, lipid metabolism or transport disorders, and viral

XX infections. These are also useful in assessing the effects of exogenous

XX compounds on the expression of nucleic acids and amino acid sequences of

XX REMAP, in facilitating drug discovery process, and in investigating the

XX pathogenesis of diseases or medical conditions. Expression and

XX purification were achieved using bacterial or virus-based expression

XX systems. The present sequence represents an REMAP protein of the

XX invention.

XX Sequence 416 AA;

RESULT 8
ADA49700
ID ADA49700 standard; protein; 170 AA.

XX ADA49700;

XX 20-NOV-2003 (first entry)

XX Extracellular region of human TNFRp (hTNFRp) protein.

XX Apo-2 ligand inhibitor; Apo-2Li; Apo-3; apoptosis; affinity;

XX competitive-type receptor; binding assay; cancer cell; human;

XX TNF receptor family; hTNFRp; cytosolic.

XX Homo sapiens.

XX US2002192729-A1.

XX 19-DEC-2002.

XX 28-MAR-2002; 2002US-00112793.

XX 01-APR-1996; 96US-00625328.

XX 23-SEP-1996; 96US-00710802.

XX 31-MAR-1997; 97US-00828683.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ;

XX WPI; 2003-657226/62.

XX Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or

XX Apo-3 polypeptide which induces or stimulates apoptotic activity, useful

XX in diagnostic assays.

XX disclosure; Fig 2; 53pp; English.

XX The present invention relates to the isolation of a biologically active

XX Apo-2 ligand inhibitor (Apo-2Li) or Apo-3, and the polynucleotide

XX sequences encoding them. Apo-2Li and Apo-3 are involved in apoptosis. The

XX Apo-2Li and Apo-3 polypeptides are useful in diagnostic assays. Apo-2Li

XX is useful for generating antibodies, as standards in assays for Apo-3 or

XX receptor binding assays when labelled with radiolabel, and in competitive-type

XX fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or

XX inducing apoptosis in cancer cells, and thus have therapeutic utility.

XX The present sequence represents the extracellular region of a human TNF

XX receptor family protein. This sequence is compared with the extracellular

XX region of human Apo-2Li.

XX Sequence 170 AA;

XX Query Match 87.1%; Score 987; DB 6; Length 170;

XX Best Local Similarity 100.0%; Pred. No. 1.2e-67;

XX Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 15 TRDQKYEYEPQHRICSRCPGTYVSACSRIRDTVCATCAENSYNHMYLTTCQIC 74

XX 1 TRDQKYEYEPQHRICSRCPGTYVSACSRIRDTVCATCAENSYNHMYLTTCQIC 60

XX 75 RCDPEVMGLEIAPCTSKRTQCRCPGFMCAAMALECHHCELLSDCPGTAELKDEVG 134

XX 61 RCDPEVMGLEIAPCTSKRTQCRCPGFMCAAMALECHHCELLSDCPGTAELKDEVG 120

XX 135 KGNNECVCKAGHFQNTSSPSARCPHTRCENQGLVEAAGTAQSDTTCK 184

XX 121 KGNNECVCKAGHFQNTSSPSARCPHTRCENQGLVEAAGTAQSDTTCK 170

XX RESULT 9

XX AAB36700

ID	Sequence	Score	DB	Length	Indels	Gaps
AAAB36700	standard; protein; 415 AA.	68.0%	771	415	2	1
AAAB36700		70.7%	844-51			
15-MAR-2001	(first entry)	14	40	2	1	
Human tumour necrosis factor receptor LTBR protein SEQ ID NO.6.						
Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nototropic; TRAIL receptor without intracellular domain; diagnosis; cytostatic; tumour necrosis factor related apoptosis inducing ligand; vasotropic; immunosuppressive; neuroprotective; antiviral; antinflammatory; anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian; gene therapy; restenosis; graft versus host disease; tumour; cancer; apoptotic cell death related disease; autoimmune disorder; cardiovascular disorder; viral infection.						
Homo sapiens.						
MO200071150-A1.						
30-NOV-2000.						
18-MAY-2000; 2000MO-US013515.						
20-MAY-1999; 99US-0135164P.						
(HUMA-) HUMAN GENOME SCI INC.						
Wei Y, Ruben SM, Gentz RL, Ni J;						
WPI; 2001-041051/05.						
Nucleic acid encoding a TRID polypeptide, also referred to as tumor necrosis factor receptor 5, useful in the diagnosis, treatment or prevention of cancer, autoimmune disorders and viral infection.						
Disclosure; Fig 2; 285pp; English.						
The present invention describes the human TRID protein (tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without intracellular domain, also referred to as tumour necrosis factor receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive, nototropic, neuroprotective, antiviral, antinflammatory, anticonvulsant, antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic activities, and can be used in gene therapy. The TRID polynucleotides are useful for detecting complementary polynucleotides. TRID proteins and polynucleotides are useful in the treatment of tumours, resistance to parasite, bacteria and viruses, restenosis and graft versus host disease. They are also useful for inducing proliferation of T-cells, endothelial cells and certain haematopoietic cells, to regulate antiviral responses and to prevent certain autoimmune diseases after stimulation of TRID by an agonist or TRAIL binding facilitator. The antibodies which bind TRID polypeptides are useful for treating and/or preventing diseases associated with increased or decreased apoptotic cell death. The TRID polynucleotides, proteins, antibodies, agonists and antagonists are useful in the diagnosis, treatment or prevention of: (a) cancer; (b) autoimmune disorders; (c) diseases associated with increased apoptosis; (d) cardiovascular disorders; and (e) viral infection. The present sequence represents a tumour necrosis factor receptor used in comparison with TRID in the exemplification of the present invention						
Sequence 415 AA;						
Query Match	68.0%	Score 771	DB 4	Length 415		
Best Local Similarity	70.7%	Pred. No. 844-51				
Matches 135; Conservative 14; Mismatches 40; Indels 2; Gaps 1;						
1 SOPQAVPAPASEKOTCRDQDEKYEYFQHIICSRCPGPGTVYSAKSRIRDTVCATCAENS 60						
28 SQQVLPPIRINQOTCMQDQKXEYRPMHVDVCCSRCPGGEFVAVVCSRSQDTVCTCKPENS 87						
61 YNEHMYLITTCQRCPCDPVMELEIAPCTSRKRTQCRQCPGFCAMALECTHC--ELL 118						

QY	DB	Sequence	Score	Length	Matches	Conservative	Mismatches	Indels	Gaps
QY	DB	119 SDPEPTGEALKDVEKGNHCVCKAGHFOHTSSPSARCOPTHRCENOGVLEAAPGTAQ	68.0%	415	148	135	14	2	1
QY	DB	179 SDTTCCKNPLEP	70.7%	51	28	15	4	0	0
QY	DB	208 SDTTCCKNPPBP	70.7%	51	28	15	4	0	0
QY	DB	1 SOPQAVPPYASNNQCRDQEKRYEPPORHICSRCPGQVYSAKSRIRDTVCATCAANS	68.0%	415	148	135	14	2	1
QY	DB	28 SOPQAVPPYRINQCTQWDDQKRYEMHADVCCSRCPGSEFVYAVACRSQDITVCKTCPOHNS	70.7%	51	28	15	4	0	0
QY	DB	61 YNEHNMVYLTICQLCPBCPDVWGLIEIAPCTSKRKTQCRQCPGMFCAMALBECTHC--ELL	70.7%	118	87	45	14	2	1

Db 88 YNEHNNHLSGTCQLCPGCIIVLGFBEVAPCTSDPRKRECCQPMSCVYIADNECVHEERRL 147
QY 119 SDGPPGTAEIKDEYKGNHNCVPCKAGHPONTSSPARCQPHTRCENOGIWEAPGTAQ 178
Db 148 VLQPGTEAEVYDEIMDTDVNCVPCPGHPONTSSPARCQPHTRCENOGIWEAPGTSY 207
QY 179 SDTCKKNPLEP 169
Db 208 SDTCKKNPPPE 218

RESULT 11

AAW94642
ID AAW94642 standard; peptide, 77 AA.

XX AAW94642;
XX 29-APR-1999 (first entry)
XX TNF-R extracellular Cys-rich domain TNF-R-IP.
XX Tumour necrosis factor receptor; TNF-R; autoimmune diseases;
XX inflammation; septic shock; cachexia; graft versus host disease;
XX skin allergic reaction; immune complex disease; malaria;
XX transplantation rejection.

OS Homo sapiens.
XX WO9853842-A1.
XX 03-DEC-1998.
XX 29-MAY-1998; 98WO-US010891.
XX 30-MAY-1997; 97US-00866545.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Greene MI, Murali R, Takasaki W;
XX WPI; 1999-080781/07.

XX New compounds designed from a binding loop of a tumour necrosis factor
XX receptor - are capable of inhibiting the biological activities of tumour
XX necrosis factor, e.g., in treating inflammation or autoimmune diseases.

XX Disclosure; Fig 1; 78pp; English.

XX The present invention describes peptides and peptide analogues which
XX correspond in primary sequence to a binding loop of a tumour necrosis
XX factor receptor (TNF-R) superfamily member. The compounds are especially
XX designed from a binding loop of TNF-R p55. They are capable of inhibiting
XX TNF binding to its cellular receptors and may be used to inhibit the
XX biological activities of TNF. They may be used in treating TNF-associated
XX conditions such as acute and chronic inflammatory responses, septic
XX shock, cachexia, autoimmunity, graft-versus-host disease, skin allergic
XX reactions, immune complex disease, transplantation rejection and malaria.
XX Administration is, e.g. oral, transdermal, transmucosal, pulmonary,
XX subcutaneous, intravenous or intramuscular. Parenteral dosage is 0.1-5
XX mg/kg/day. The present sequence represents an extracellular Cys-rich
XX domain of TNF-R from the present invention

XX Sequence 77 AA;

Query Match 40.2%; Score 456; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.5e-27;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNHNNYLTICQLCRPCDPVWGIEFIAPCTSKRKTQCRCPGMFCAMALE 111
Db 1 VCATCAENSYNHNNYLTICQLCRPCDPVWGIEFIAPCTSKRKTQCRCPGMFCAMALE 60

QY 112 CTHCELLSDCPGTAE 128
Db 61 CTHCELLSDCPGTAE 77

RESULT 12

AAB69194
ID AAB69194 standard; protein, 77 AA.

XX AAB69194;
XX 30-APR-2001 (first entry)

XX Human TNF-R extracellular Cys-rich domain TNF-R-IP SEQ ID NO:3.
XX Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;
XX osteoclastogenesis; bone loss; bone resorption; osteoporosis;
XX anti-rheumatic; antiarthritic; antiinflammatory; immunomodulatory;
XX tumour necrosis factor-related activation-induced cytokine; TRANCE;
XX receptor activator of NF-kappaB ligand; RANK; osteoporosis;
XX Paget's disease; metastatic bone disease; rheumatoid arthritis;
XX periodontal disease; modulating dendritic cell maturation;
XX T cell proliferation; CD40 receptor system.

XX Homo sapiens.
XX WO200108699-A1.
XX 08-FEB-2001.
XX 28-JUL-2000; 2000WO-US020510.
XX 28-JUL-1999; 99US-0146090P.

XX (UYPE-) UNIV PENNSYLVANIA.
XX (AOKI/) AOKI K.
XX (HORN/) HORNE W C.
XX (BARO/) BARON R.
XX Aoki K, Horne WC, Baron R, Greene MI, Murali R;
XX WPI; 2001-182866/18.

XX Use of peptides and peptide analogs which are TRANCE/RANK inhibitors, for
XX inhibiting osteoclastogenesis and bone resorption.
XX Disclosure; Fig 1; 81pp; English.

XX The present invention describes a method for inhibiting
XX osteoclastogenesis and bone resorption. Osteoclastogenesis and bone
XX resorption inhibiting peptide analogues from the present invention have
XX osteoparaphic, cytostatic, antirheumatic, antiarthritic, antiinflammatory
XX and immunomodulatory activities, and are tumour necrosis factor (TNF)-
XX kappaB ligand (RANK) inhibitors. The method is useful for treating
XX disease characterised by bone loss such as osteoporosis, Paget's
XX disease, metastatic bone disease, rheumatoid arthritis or periodontal
XX disease, and modulating dendritic cell maturation, T cell proliferation,
XX and/or CD40 receptor systems. The present sequence represents an
XX extracellular Cys-rich domain of a tumour necrosis factor receptor (TNF-
XX R) superfamily member, which is used in the exemplification of the
XX present invention

XX Sequence 77 AA;

Query Match 40.2%; Score 456; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.5e-27;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VCATCAENSYNHNNYLTICQLCRPCDPVWGIEFIAPCTSKRKTQCRCPGMFCAMALE 111
Db 1 VCATCAENSYNHNNYLTICQLCRPCDPVWGIEFIAPCTSKRKTQCRCPGMFCAMALE 60

QY 112 CTHCELLSDCPPTGEAF 128
 Db 61 CTHCELLSDCPPTGEAF 77

RESULT 13

ABP41926 ID ABP41926 standard; protein; 305 AA.

XX ABP41926;

DT 22-AUG-2002 (first entry)

XX Human ovarian antigen HSABJ44, SEQ ID NO:3058.

XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KM ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KM infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KM PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KM inflammatory condition; immune disorder; blood disorder;
 KM cardiovascular disorder; respiratory disorder; neurological disorder;
 KM gastrointestinal disorder; urinary system disorder; drug screening;
 KM gene therapy; chromosome mapping; forensic analysis;
 KM antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KM antiinflammatory; gynaecological; reproductive; chromosome 12p13.

XX Homo sapiens.

XX WO200200677-A1.

XX 03-JAN-2002.

XX 07-JUN-2001; 2001WO-US018569.

XX 07-JUN-2000; 2000US-0209467P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX MPI; 2002-147878/19.

XX N-PSDB; AB055003.

XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.

XX Claim 11; SEQ ID NO 3058; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovarian and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the

CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 305 AA;

Query Match 33.7%; Score 381.5; DB 5; Length 305;
 Best Local Similarity 93.4%; Pred. No. 2,9e-21;
 Matches 71; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 123 PGTEA-ELKDEVGKGNHCVCKAGHPONTSPSPARCOPTRENOGLVEAAPGTASDT 181

Db 19 PGMPALFLPPEVKGKNNHCPCAKGHHQNTSSPSARCOPTRENOGLVEAAPGTASDT 78

QY 182 TCKNPLELPPEMSGT 197

Db 79 TCKNPLELPPEMSGT 94

RESULT 14

AAR51003 ID AAR51003 standard; protein; 518 AA.

XX AAR51003;

XX 25-MAR-2003 (revised)

DT 07-OCT-1994 (first entry)

XX Sequence of a recombinant human (rhu) tumour necrosis factor receptor

DE TNFR/Fc fusion protein.

XX Tumour necrosis factor receptor; chimeric antibody molecule;

XX immunoglobulin.

XX Synthetic.

XX WO9406476-A1.

XX 31-MAR-1994.

XX 14-SEP-1993; 93WO-US008666.

XX 15-SEP-1992; 92US-00946236.

XX (IMMV) IMMUNEX CORP.

XX Smith CA, Jacobs CA;

XX MPI; 1994-118172/14.

XX N-PSDB; AA045225.

XX Treating TNF mediated inflammatory diseases with TNF antagonist - esp.

PT soluble form of TNF receptor, opt. as fusion protein with human

PT immunoglobulin Fc region, esp. for treating arthritis.

XX Disclosure; Page 32-34; 47pp; English.

XX AA045224 is cDNA from clone 1 of library WI-26 V4 of human fibroblast
 CC cell line WI-26 V4. The mature full-length TNFR1 is a glycoprotein
 CC having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for TNFR1
 CC was described in Smith et al., Science 248:1019,1990. Clone 1 is
 CC contained in expression vector pCAV/NOT-TNFR (ATCC 68088). A recombinant
 CC chimeric antibody may be produced having TNFR sequences substituted for
 CC the variable domains of either or both of the immunoglobulin molecule
 CC heavy and light chains and having unmodified constant region domains. A
 CC specific example of a TNFR/Fc fusion protein is given in AA045225/R51003.
 CC The rhu TNFR/Fc fusion gene was created by ligating the following
 CC fragments into a cloning vector: 1) an 867 bp Asp718-Pvu2 fragment from
 CC pCAV/NOT-TNFR (ATCC 68088) contg. the cDNA encoding the truncated TNFR.
 CC 2) a 700 bp StyI-SpeI fragment from plasmid pIX498 coding for 232 AAs of

CC the Pc portion of human IgG1. Plasmid pIXY498 is a yeast expression
CC vector contg. the Pc fragment of human IgG1.3) An oligo linker, to fuse
CC the truncated TNFR with the human IgG1 Pc fragment. This linker was
CC created by PCR using primer AAQ45226, which encodes the 3' end of the
CC truncated TNF receptor and the 5' end of human IgG1, and primer AAQ45227,
CC which is an antisense sequence encoding bps 257-237 of human IgG1.
CC (Updated on 25-MAR-2003 to correct PM field.)
XX

SQ Sequence 518 AA;

Query Match 27.8%; Score 315; DB 2; Length 518;
Best Local Similarity 35.5%; Pred. No. 5.9e-16;
Matches 71; Conservative 24; Mismatches 77; Indels 28; Gaps 9;

QY 5 AVPPYASE-NQTCDEKEYEYEPQHRICCSRCPPGTIVSAKCSIRIDTCATCAENS YNE 63
Db 57 AFTFYAPEPGSTCR--LREYYDQTAQWCCSKSPGHAKVFCRTKTSPTVCDSCEDSYTYQ 114
64 HNNVLTICOLCR---PCDPYMGLEIAPCTSKRKTQCRQCPGMFCAMALE-CTHCELLS 119
Db 115 IMNWVPECLSCGSRCSQDV---ETQACTREQNRICTCRPGWYCALSKQEGRLCAPLR 170
QY 120 DCPFG-----TEALKDEVGKGNHCVPCKAGHFONTSSPSARCOPTTRCENOGIVEAP 174
Db 171 KCRPFGVAPRGTEISDVV-----CKPCAPGTFSNTSTSDICRPHQICN----VVAIP 220
QY 175 GTAQSDPTTC--KNPLELPP 192
Db 221 GNASMDAVCTSTSTPSRMAP 240

RESULT 15

ABJ37103
ID ABJ37103 standard; protein; 659 AA.

XX ABJ37103;

DT 08-MAY-2003 (first entry)

DE Concatameric immunoadhesion human protein sequence SEQ ID No 12.

XX Antinflammatory; antibacterial; immunosuppressive; antirheumatic;
XX antiarthritic; immunomodulator; concatameric protein; soluble domain;
XX dimeric protein; inflammation; septicemia; cytotoxicity;
XX rheumatoid arthritis; cachexia; inflammation; human.

OS Homo sapiens.

XX WO2003010202-A1.

PD 06-FEB-2003.

PF 26-JUL-2002; 2002WO-KR001427.

PR 26-JUL-2001; 2001KR-00045028.

PA (MEDE-) MEDEXGEN CO LTD.

PI Chung Y, Han J, Lee H, Choi E, Kim J,

DR WPI; 2003-229639/22.

DR N-PSDB; ABT32046.

XX New concatameric protein having two soluble domains, useful for
PT diagnosing and treating disorders associated with the dimeric protein or
PT its glycosylated form, such as inflammation, septicemia, rheumatoid
PT arthritis and cachexia.

PS Claim 27; Page 148-152; 211pp; English.

XX The invention relates to a novel concatameric protein comprising two
CC soluble domains, in which an N-terminus of a soluble domain of a
CC biologically active protein is linked to a C-terminus of an identical

CC soluble domain or a different soluble domain of a biologically active
CC protein. The methods and compositions of the present invention are useful
CC for the diagnosis and treatment of disorders associated with dimeric
CC protein or its glycosylated form, such as inflammation, septicemia,
CC cytotoxicity, rheumatoid arthritis, cachexia and other inflammation-
CC related diseases. This sequence represents the human concatameric protein
CC of the invention
XX

SQ Sequence 659 AA;

Query Match 27.5%; Score 311.5; DB 6; Length 659;
Best Local Similarity 36.4%; Pred. No. 1.4e-15;
Matches 71; Conservative 23; Mismatches 74; Indels 27; Gaps 9;

QY 5 AVPPYASE-NQTCDEKEYEYEPQHRICCSRCPPGTIVSAKCSIRIDTCATCAENS YNE 63
Db 28 AFTFYAPEPGSTCR--LREYYDQTAQWCCSKSPGHAKVFCRTKTSPTVCDSCEDSYTYQ 85
64 HNNVLTICOLCR---PCDPYMGLEIAPCTSKRKTQCRQCPGMFCAMALE-CTHCELLS 119
Db 86 IMNWVPECLSCGSRCSQDV---ETQACTREQNRICTCRPGWYCALSKQEGRLCAPLR 141
QY 120 DCPFG-----TEALKDEVGKGNHCVPCKAGHFONTSSPSARCOPTTRCENOGIVEAP 174
Db 142 KCRPFGVAPRGTEISDVV-----CKPCAPGTFSNTSTSDICRPHQICN----VVAIP 191
QY 175 GTAQSDPTTC--KNPLEP 189
Db 192 GNASMDANCTSP-EP 205

Search completed: August 27, 2004, 21:07:57
Job time : 135 secs

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OM protein - protein search, using sw model

Run on: August 27, 2004, 21:02:27 ; Search time 115 Seconds

(without alignments)
540.496 Million cell updates/sec

Title: US-09-626-219-1

Perfect score: 1133

Sequence: 1 SQPQAVPYASENQTCDPQE.....QSDTTCNPLPPLPPMSGT 197

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_ivirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	309.5	27.3	483	13	Q800K7
2	295.5	26.1	278	6	Q8SQ34
3	291.5	25.7	433	11	Q912M6
4	291.5	25.7	474	11	Q80MY6
5	290	25.6	459	11	Q62327
6	284.5	25.1	274	6	Q7YRL5
7	278	24.5	223	4	Q86TK5
8	276.5	24.4	482	11	Q88734
9	265.5	23.4	277	6	Q8WMQ2
10	258	22.8	275	11	Q80WM9
11	253	22.3	462	13	Q805B0
12	243.5	21.5	289	11	Q8K2X6
13	242.5	21.4	283	6	Q9X8Z8
14	240	21.2	186	12	Q72735
15	238.5	21.1	318	13	Q7E2H3
16	238	21.0	302	13	Q9PUS0

17	233.5	20.6	457	4	Q81VS6	Q81VS6 homo sapien
18	232.5	20.5	467	13	Q80010	Q80010 gallus galli
19	230	20.3	276	13	Q9DDD2	Q94442 gallus galli
20	230	20.3	351	12	Q57117	Q57117 cowpox viru
21	229.5	20.3	285	12	Q90W71	Q90W71 oncorhynch
22	226.5	20.0	167	12	Q80Y13	Q80Y13 vaccinia vi
23	225.5	19.9	186	13	Q72ZY5	Q72ZY5 gallus galli
24	225.5	19.9	651	13	Q98SM6	Q98SM6 gallus galli
25	225	19.9	186	12	Q9YPR7	Q9YPR7 cowpox viru
26	225	19.9	349	12	Q57099	Q57099 monkeypox v
27	225	19.9	349	12	Q57098	Q57098 monkeypox v
28	225	19.9	349	12	Q57284	Q57284 camelipox vi
29	223	19.7	186	12	Q911R5	Q911R5 vaccinia vi
30	221.5	19.5	285	13	Q90YS6	Q90YS6 oncorhynch
31	221	19.5	349	12	Q57100	Q57100 monkeypox v
32	221	19.5	349	12	Q57097	Q57097 monkeypox v
33	220.5	19.5	166	11	Q9UKB0	Q9UKB0 rattus norv
34	219	19.3	349	12	Q57102	Q57102 monkeypox v
35	219	19.3	349	12	Q57291	Q57291 monkeypox v
36	218.5	19.3	167	12	Q9DJL2	Q9DJL2 cowpox viru
37	218.5	19.3	350	12	Q57116	Q57116 cowpox viru
38	218	19.2	186	12	Q9W7B4	Q9W7B4 vaccinia vi
39	218	19.2	348	12	Q57108	Q57108 monkeypox v
40	218	19.2	348	12	Q57103	Q57103 monkeypox v
41	217.5	19.2	267	6	Q02764	Q02764 oryctolagus
42	216.5	19.1	167	12	Q72762	Q72762 cowpox viru
43	216	19.1	348	12	Q57277	Q57277 monkeypox v
44	216	19.1	349	12	Q57101	Q57101 monkeypox v
45	210	18.5	348	12	Q57112	Q57112 variola vir

ALIGNMENTS

RESULT 1

Q800K7 PRELIMINARY; PRT; 483 AA.
ID Q800K7
AC Q800K7
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumor necrosis factor receptor-2.
GN TNFR-2.
OS Paratichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paratichthyidae; Paratichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Park C., Kurobe T., Hirano I., Aoki T.;
RT "Cloning and characterization of cDNAs for two distinct tumor necrosis
factor receptor superfamily genes from Japanese Flounder Paratichthys
RT olivaceus."
RU Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB080947; BAC65226.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 3.
KW Receptor.
SQ
SEQUENCE 483 AA; 52227 MW; EE55874A8C7F2085 CRC64;

Query Match 27.3%; Score 309.5; DB 13; Length 483;
Best Local Similarity 35.4%; Pred. No. 2.9e-25;

Matches 64; Conservative 20; Mismatches 80; Indels 17; Gaps 6;

QY 16 GSDQKEYEPGRKCCRCPRGTVSAKCSIRITVCATCAENSYNEHMYLTTCQLCR 75
DB 27 CHNSTEYRED--LCCKCPGGRLLQCKSDATESVCKQCDSDGQYMERKNYAQKCLSCN 84

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OY 76 PCDPVWGLEIAPCTSKRKTCRCOPGMFCAMALE-----CHCELLSDCPPTAEIK 130
DB 85 KCSNNGILOYAGRCSSPTRTGCVCKRPMYC---IMFDNPYCAECNYSQCRAGYVSLP 141
OY 131 DEVGKGN--HCVPCKAGHFOUNTSSPARCOPHTRCNOCGLVEAPGTASDPTCKNPLE 188
DB 142 ---GKANSDVKCELCPPGMSNTSSNTETCRPHDCHGKAVR--KNTTSDIVCEBGVA 196
OY 189 P 189
DB 197 P 197

RESULT 2
OBSQ34 PRELIMINARY; PRT; 278 AA.
AC OBSQ34, 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE CD40.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN (1)
RP SEQUENCE FROM N.A.
RA West K.A., Li A.W., Rowden G.;
RT "Characterization of the Porcine CD40 Molecule."
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF248545; AAL2924.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR GO; GO:0008063; P:faa receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
SQ SEQUENCE 278 AA; 30951 MW; 20D446E4AF93DD2 CRC64;

Query Match 26.1%; Score 295.5; DB 6; Length 278;
Best Local Similarity 36.9%; Pred. No. 5.4e-24;
Matches 62; Conservative 19; Mismatches 74; Indels 13; Gaps 3;

OY 21 KEYEPQHRICSSRCPPGTYSAKCSRIDTVCATCAENSYEHNNYLTICQLCRPCDPV 80
DB 27 KENQVPTNSRCNLCPPGQKLVNHCTEVEETELPCSSSEFLATNMRKHCHQHKYCDN 86
OY 81 MGLERIAPCTSKRKTCRCOPGMFCAMALECHCELLSDCPG-----TEAELKDEVGK 135
DB 87 LGLQVQREGSTSLDTTTCVSEBHHCTNSA--CESCTLHLDFCLPGGLVKQMAIEVSTI-- 142
OY 136 GNNHCVPCKAGHFOUNTSSPARCOPHTRCNOCGLVEAPGTASDPTTC 183
DB 143 ----CPCPVGPFNSNVSASEKQPTWSCSKGLVQRAGTNTDVVC 186

RESULT 3
OBSQ34 PRELIMINARY; PRT; 433 AA.
AC OBSQ34, 01-JUN-2002 (Tremblrel. 19, Created)
DT 01-JUN-2002 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Tumor necrosis factor receptor type II (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley;
RA Oburg B., Pelser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT capillary endothelial cells and participate in TNF-alpha transport
RT through the blood-brain barrier."
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF420214; AAL16021.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR KEGG; K04462; TNFR_NGFR_2; 3.
FT NON_TER 1
FT NON_TER 433
SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

Query Match 25.7%; Score 291.5; DB 11; Length 433;
Best Local Similarity 33.3%; Pred. No. 2.3e-23;
Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;

OY 8 PYASNOTCDQKEYEYEPQHRICSSRCPPGTYSAKCSRIDTVCATCAENSYEHNNY 67
DB 11 PYKEPQNGQOISQEIYDKKQWCAKCPGQYAKHFCKNTSDIVCAACAGMFTQWNH 70
OY 68 LTTICQLCRPC--DPVWGLEIAPCTSKRKTCRCOPGMFCA--AMALECHCELLSDCP 122
DB 71 LHTCLSCSSSCSDQV---ETHNCTKQNVCACMADSYALKLHSGNCQCKLSCG 126
OY 123 PGTAEIKDEVGKNNHCVPCKAGHFOUNTSSPARCOPHTRCNOCGLVEAPGTASDPT 182
DB 127 PGF-GVARSRTSNNAVICSACAPGTFSDTTSITDVCRRHRICS-----ILAIQNASSTAV 181
OY 183 CKNPLEPLPPPMSCGT 197
DB 182 CASE-SPTPSAVPRT 195

RESULT 4
OBSQ36 PRELIMINARY; PRT; 474 AA.
AC OBSQ36, 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Tumor necrosis factor receptor type II.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=Wistar; TISSUE=Spleen;
RA Li Y., Ji A., Schaefer M.K.;
RT "Expression of TNFR2 in rat dorsal root ganglion."
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF498039; AAP3151.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR_4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
DR KEGG; K04462; TNFR_NGFR_2; 3.
SQ SEQUENCE 474 AA; 50148 MW; 298C6AB9E8C8D714 CRC64;

Query Match 25.7%; Score 291.5; DB 11; Length 474;
Best Local Similarity 33.3%; Pred. No. 2.6e-23;

```

Matches 65; Conservative 24; Mismatches 91; Indels 15; Gaps 7;

QY PYASENQTCDQEKYEYEPQHRICSRCPGGTVASAKCSIRIDTVCATCAENSNEYHMY 67
 Db 31 PYKPEPGNQCQISQYDYKKAQMCACPCPGQYAHFPCNKTSIDTVCACCAAMFTQVWNH 90
 QY 68 LTIICQLC-RPC--DPVWGLGEIAPCTSKRTQRCQPGMFCA--AMALECTHCELLSDCP 122
 Db 91 LHTICLSSSSCSDDQV---ETHNCTKKQNRVCAQMAQSYCALKIHSGNCRQCKLSKCG 146
 QY 123 PGTEALIKDEVKGNHNCVPCKAGHFQNTSSPSARCPHTRCENOGIVEAAPGTASDPT 182
 Db 147 PGF-GVAASRTSNGNVICACAPGTSTSTVCRPHRICS---TLALPGASTDAY 201
 QY 183 CKNPLEPLPPPEWSGT 197
 Db 202 CASE-SPTPSAVPT 215

RESULT 5
 Q62327
 ID Q62327 PRELIMINARY; PRT; 459 AA.
 AC Q62327;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Murine tumour necrosis factor receptor 2 protein (Fragment).
 GN TMRFR51B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBL_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD;
 RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
 RT "Amino acid variation in the tumor Necrosis factor receptor 2 is
 RL linked to autoimmune diabetes in NOD mice."; Genomics 0:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD;
 RA MEDLINE=95178848; PubMed=7873884;
 RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
 RT "Allelic variation of the type 2 tumor necrosis factor receptor
 RL gene."; Mamm. Genome 5:726-727 (1994).
 DR EMBL: X76401; CAAS3981.1; --
 DR PIR: I48854; I48854.
 DR HSSP: P19438; INCF.
 DR MGD: MGI:1314883; Tnftr51b.
 DR GO: GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.
 DR GO: GO:0006954; P:inflammatory response; IMP.
 DR GO: GO:0008220; P:necrosis; IMP.
 DR InterPro: IPR001368; TMRFR_6.
 DR Pfam: PF00020; TMRFR_6; 4.
 DR SMART: SMO0208; TMRFR_6; 4.
 DR PROSITE: PS00652; TMRFR_NGFR_1; 2.
 DR PROSITE: PS50050; TMRFR_NGFR_2; 3.
 KM Receptor.
 FT NON_TER 1
 FT VARIANT 87 1
 FT VARIANT 93 87 S -> T.
 FT VARIANT 93 93 T -> I.
 FT VARIANT 268 268 F -> I.
 FT VARIANT 345 345 S -> F.
 FT VARIANT 421 421 Y -> C.
 SQ SEQUENCE 459 AA; 48686 MM; 6C51D2CF1C4626DF CRC64;
 Query Match 25.6%; Score 290; DB 11; Length 459;
 Best Local Similarity 33.5%; Pred. No. 3,6e-23;
 Matches 65; Conservative 24; Mismatches 85; Indels 20; Gaps 8;
 QY 8 PYASE-NOTCDQEKYEYEPQHRICSRCPGGTVASAKCSIRIDTVCATCAENSNEYHMY 66

Db 16 PYKEPEGYEQCISQ-EYDRAQMCACPCPGQYKHKCNNTSDTVCACDCAAMTQVWN 74
 QY 67 YLTIICQLC---PCDPVWGLGEIAPCTSKRTQRCQPGMFCA--AMALECTHCELLSDC 121
 Db 75 QPRTICLSSSSCSSTQV---ETRACTKQNRVCAQMAQSYCALKIHSGNCRQCKLSKCG 130
 QY 122 PGTEALIKDEVKGNHNCVPCKAGHFQNTSSPSARCPHTRCENOGIVEAAPGTASDPT 181
 Db 131 PGF-GVAASRTSNGNVICACAPGTSTSTVCRPHRICS---TLALPGASTDAY 185
 QY 182 CKNPLEPLPPPEWS 195
 Db 186 VC---APESPTLS 195

RESULT 6
 Q7YRL5
 ID Q7YRL5 PRELIMINARY; PRT; 274 AA.
 AC Q7YRL5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CD40.
 GN CD40.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RX NCBL_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang S., Sim G.-K.;
 RT "Canine CD40 and CD40 ligand cDNA Sequences";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY333789; AAP8653.1; --
 SQ SEQUENCE 274 AA; 30284 MM; 9723789A07FAB6DB CRC64;

Query Match 25.1%; Score 284.5; DB 6; Length 274;
 Best Local Similarity 34.9%; Pred. No. 8,4e-23;
 Matches 61; Conservative 18; Mismatches 89; Indels 7; Gaps 4;

QY 9 PYASENQTCDQEKYEYEPQHRICSRCPGGTVASAKCSIRIDTVCATCAENSNEYHMY 68
 Db 19 YPEPRYACR--EKQYLVDSQ--CNMCPGEXKLVNDCLHTIDTCRCQGTGERLDTWNAE 74
 QY 69 TICQCRPCDPVWGLGEIAPCTSKRTQRCQPGMFCAAMALECTHCELLSDCPGTAE 128
 Db 75 RHCHQHKICDPVWGLHVEKXGTSITDTTCDEGJHCTNAA--CESCTWHSICPGLGVK 132
 QY 129 LKDEVKGNHNCVPCKAGHFQNTSSPSARCPHTRCENOGIVEAAPGTASDPTC 183
 Db 133 QIATGISDITDPCPIGFFSVSALRKCHWTSCETGLVKQAGINKTIVIC 186

RESULT 7
 Q86YK5
 ID Q86YK5 PRELIMINARY; PRT; 223 AA.
 AC Q86YK5;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 5 (Fragment).
 GN TNFRSF5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 RX NCBL_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA He X., Xu L., Zeng Y.;
 RT "Transcripts of CD40 isoform in peripheral mononuclear cells";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY225405; AA043990.1; --

DR GO:0016020; C:membrane; IEA.
 DR GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO:0005488; F:binding; IEA.
 DR GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO:0006915; P:apoptosis; IEA.
 DR GO:0006955; P:immune response; IEA.
 DR GO:0007165; P:signal transduction; IEA.
 DR GO:0006810; P:transport; IEA.
 DR InterPro:IPR006209; EGF like.
 DR InterPro:IPR008063; Fas receptor.
 DR InterPro:IPR001993; Mitochond carrier.
 DR InterPro:IPR001368; TNFR_c6.
 DR Pfam:PF00020; TNFR_c6; 4.
 DR PRINTS:PRO1680; FASRECEPTOR.
 DR SMART:SM00208; TNFR; 4.
 DR PROSITE:PS01186; EGF_2; 1.
 DR PROSITE:PS00215; MITOCH_CARRIER; 1.
 DR PROSITE:PS00652; TNFR_NGFR_1; 1.
 DR PROSITE:PS50050; TNFR_NGFR_2; 4.
 DR Receptor.
 KM NON TER 223
 SQ SEQUENCE 223 AA; 24659 MW; 85C63C20BC4E0B1C CRC64;

Query Match 24.5%; Score 278; DB 4; Length 223;
 Best Local Similarity 35.0%; Pred. No. 3.5e-22;
 Matches 62; Conservative 20; Mismatches 83; Indels 12; Gaps 5;

QY 7 PPVASENQTORDQDEKEYEYEPQHRCICSRCPPTGVSAKCSRIRDTVCATCAENSYNEHWN 66
 ID 088734 PRELIMINARY; PRT; 482 AA.
 AC 088734;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DT P80 TNF-alpha receptor.
 GN TNFR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CC NCBI_TaxId=10090;
 OK NCBI_TaxId=10090;
 RX MEDLINE:98414512; PubMed:9740674;
 RA Hurler B., Segade F., Rodriguez R., Ramos S.S., Iazo P.S.;
 RT "The Mouse Tumor Necrosis Factor Receptor 2 Gene: Genomic Structure
 and Characterization of the two Transcripts";
 RT Genomics 52:79-98(1998).
 RL EMBL:Y14619; CAA74969.1; -
 DR EMBL:Y14620; CAA74969.1; JOINED.
 DR EMBL:Y14621; CAA74969.1; JOINED.
 DR EMBL:Y14622; CAA74969.1; JOINED.
 DR EMBL:Y14623; CAA74969.1; JOINED.
 DR EMBL:Y14624; CAA74969.1; JOINED.
 DR HSSP:Q92956; IUMA.
 DR GO:0004872; F:receptor activity; IEA.
 DR InterPro:IPR001368; TNFR_c6.
 DR Pfam:PF00020; TNFR_c6; 4.
 DR SMART:SM00208; TNFR; 4.
 DR PROSITE:PS00652; TNFR_NGFR_1; 2.
 DR PROSITE:PS50050; TNFR_NGFR_2; 3.

KM Receptor.
 SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C CRC64;

Query Match 24.4%; Score 276.5; DB 11; Length 482;
 Best Local Similarity 32.3%; Pred. No. 1.1e-21;
 Matches 65; Conservative 24; Mismatches 85; Indels 27; Gaps 9;

QY 8 PPAASENQTORDQDEKEYEYEPQHRCICSRCPPTGVSAKCSRIRDTVCATCAENSYNEHWN 59
 ID 088734 PRELIMINARY; PRT; 277 AA.
 AC 088734;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Membrane protein CD40 (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI_TaxId=9940;
 GN [1]
 RT SEQUENCE FROM N.A.
 RA Zawitkowski M.S., Russ G.R., Krishnan R.;
 RT "Cloning and expression of the ovine CD40 molecule and the inhibition
 of the mixed lymphocyte reaction by the ovine CD40-BGFP fusion
 protein";
 RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
 RL EMBL:AY072798; AAL68402.1; -
 DR GO:0016020; C:membrane; IEA.
 DR GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO:0006915; P:apoptosis; IEA.
 DR GO:0006955; P:immune response; IEA.
 DR GO:0007165; P:signal transduction; IEA.
 DR InterPro:IPR008063; Fas receptor.
 DR InterPro:IPR001368; TNFR_c6.
 DR Pfam:PF00020; TNFR_c6; 4.
 DR PRINTS:PRO1680; FASRECEPTOR.
 DR SMART:SM00208; TNFR; 4.
 DR PROSITE:PS00652; TNFR_NGFR_1; 1.
 DR PROSITE:PS50050; TNFR_NGFR_2; 1.
 KM NON TER 277
 SQ SEQUENCE 277 AA; 30465 MW; 619F28BEA18A0D29 CRC64;

Query Match 23.4%; Score 265.5; DB 6; Length 277;
 Best Local Similarity 33.7%; Pred. No. 1e-20;
 Matches 56; Conservative 21; Mismatches 80; Indels 9; Gaps 4;

QY 20 EKEYEYEPQHRCICSRCPPTGVSAKCSRIRDTVCATCAENSYNEHWNLTICQCRPDP 79
 ID 088734 PRELIMINARY; PRT; 277 AA.
 AC 088734;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Membrane protein CD40 (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI_TaxId=9940;
 GN [1]
 RT SEQUENCE FROM N.A.
 RA Zawitkowski M.S., Russ G.R., Krishnan R.;
 RT "Cloning and expression of the ovine CD40 molecule and the inhibition
 of the mixed lymphocyte reaction by the ovine CD40-BGFP fusion
 protein";
 RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
 RL EMBL:AY072798; AAL68402.1; -
 DR GO:0016020; C:membrane; IEA.
 DR GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO:0006915; P:apoptosis; IEA.
 DR GO:0006955; P:immune response; IEA.
 DR GO:0007165; P:signal transduction; IEA.
 DR InterPro:IPR008063; Fas receptor.
 DR InterPro:IPR001368; TNFR_c6.
 DR Pfam:PF00020; TNFR_c6; 4.
 DR PRINTS:PRO1680; FASRECEPTOR.
 DR SMART:SM00208; TNFR; 4.
 DR PROSITE:PS00652; TNFR_NGFR_1; 1.
 DR PROSITE:PS50050; TNFR_NGFR_2; 1.
 KM NON TER 277
 SQ SEQUENCE 277 AA; 30465 MW; 619F28BEA18A0D29 CRC64;

QY 80 EKEYEYEPQHRCICSRCPPTGVSAKCSRIRDTVCATCAENSYNEHWNLTICQCRPDP 79
 ID 088734 PRELIMINARY; PRT; 277 AA.
 AC 088734;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Membrane protein CD40 (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI_TaxId=9940;
 GN [1]
 RT SEQUENCE FROM N.A.
 RA Zawitkowski M.S., Russ G.R., Krishnan R.;
 RT "Cloning and expression of the ovine CD40 molecule and the inhibition
 of the mixed lymphocyte reaction by the ovine CD40-BGFP fusion
 protein";
 RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
 RL EMBL:AY072798; AAL68402.1; -
 DR GO:0016020; C:membrane; IEA.
 DR GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO:0006915; P:apoptosis; IEA.
 DR GO:0006955; P:immune response; IEA.
 DR GO:0007165; P:signal transduction; IEA.
 DR InterPro:IPR008063; Fas receptor.
 DR InterPro:IPR001368; TNFR_c6.
 DR Pfam:PF00020; TNFR_c6; 4.
 DR PRINTS:PRO1680; FASRECEPTOR.
 DR SMART:SM00208; TNFR; 4.
 DR PROSITE:PS00652; TNFR_NGFR_1; 1.
 DR PROSITE:PS50050; TNFR_NGFR_2; 1.
 KM NON TER 277
 SQ SEQUENCE 277 AA; 30465 MW; 619F28BEA18A0D29 CRC64;

QY 138 NHCVCKAGHPONTSSPSARCPHTRCENGLVEAARGTASDTTC 183
 ID 088734 PRELIMINARY; PRT; 277 AA.
 AC 088734;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Membrane protein CD40 (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI_TaxId=9940;
 GN [1]
 RT SEQUENCE FROM N.A.
 RA Zawitkowski M.S., Russ G.R., Krishnan R.;
 RT "Cloning and expression of the ovine CD40 molecule and the inhibition
 of the mixed lymphocyte reaction by the ovine CD40-BGFP fusion
 protein";
 RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
 RL EMBL:AY072798; AAL68402.1; -
 DR GO:0016020; C:membrane; IEA.
 DR GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO:0006915; P:apoptosis; IEA.
 DR GO:0006955; P:immune response; IEA.
 DR GO:0007165; P:signal transduction; IEA.
 DR InterPro:IPR008063; Fas receptor.
 DR InterPro:IPR001368; TNFR_c6.
 DR Pfam:PF00020; TNFR_c6; 4.
 DR PRINTS:PRO1680; FASRECEPTOR.
 DR SMART:SM00208; TNFR; 4.
 DR PROSITE:PS00652; TNFR_NGFR_1; 1.
 DR PROSITE:PS50050; TNFR_NGFR_2; 1.
 KM NON TER 277
 SQ SEQUENCE 277 AA; 30465 MW; 619F28BEA18A0D29 CRC64;

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DB 141 TICEPCPVGFSSVSAFEKCHPMTSCERKGLVEGHVGNKTKDAVC 186
RESULT 10
ID Q80MM9 PRELIMINARY; PRT; 275 AA.
AC Q80MM9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 14 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=Thymus;
RA Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos G.;
RT "Light regulation in a murine model of ovarian carcinoma.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY264405; AA089081.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR008063; Fas_receptor.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR PRINTS: PRO1680; FASRECEPTOR.
DR SMART: SM00208; TNFR_4.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
DR Receptor; Signal.
KM SIGNAL
FT SIGNAL
SQ SEQUENCE 275 AA; 30171 MW; C4A7EAD8EF0C521D CRC64;

Query Match 22.8%; Score 258; DB 11; Length 275;
Best Local Similarity 34.8%; Pred. No. 6.6e-20;
Matches 63; Conservative 14; Mismatches 86; Indels 18; Gaps 6;

QY 11 SENQTRDQKEEYEPQHRICSRCPGTVSAKCSIRDTVCATCAENSYNEMNYLT 70
DB 37 SAQPSROBEFLVGD---CCYMCNPGHVKQVCEHRTGTVCAPPPQTYTAHANGLSK 92
QY 71 COLCRDPPVWGLIEIAPCTSKRKTKQRCQCPGFCAM--ALBCTHCELLSDCPGTEBEL 129
DB 93 CLPCGVCDPDMGLLTWQECSSWMDTVCRCLPGYFCENQGSHTCGLQHTTCPPQGRVE 151
QY 130 KQEVKGNNH-----CVPCKAGHFQNTSSPSARCCPHTRCENQGLVEAAPGTAQSDTTCK 184
DB 152 -----KRGTHDDTVACDLTGTG--SLGGTQEBCLFWTNC--SAFQQEVARRGNTSDTTCS 204
QY 185 N 185
DB 205 S 205

RESULT 11
Q805B0 PRELIMINARY; PRT; 462 AA.
ID Q805B0;
AC Q805B0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor necrosis factor receptor-II.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.

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OX NCBI_TaxID=9031;
RN [1]
RC SEQUENCE FROM N.A.
RA Sayde A.A.; Horuchi H., Furusawa S., Matsuda H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn H-B15; TISSUE=Spleen;
RA Sayde A., Horuchi H., Furusawa S., Matsuda H.;
RT "Molecular cloning and characterization of chicken Tumor necrosis
RT factor receptor-II (TNFR-II) and Tumor necrosis factor receptor
RT associated factor-5 (TRAF-5) genes.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB101004; BAC5966.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR008063; Fas_receptor.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR PRINTS: PRO1680; FASRECEPTOR.
DR SMART: SM00208; TNFR_4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
DR Receptor.
KM SIGNAL
SQ SEQUENCE 462 AA; 50141 MW; 8B00A93305414782 CRC64;

Query Match 22.3%; Score 253; DB 13; Length 462;
Best Local Similarity 29.4%; Pred. No. 3.9e-19;
Matches 59; Conservative 24; Mismatches 100; Indels 18; Gaps 6;

QY 8 PYASENQTRDQKEEYEPQHRICSRCPGTVSAKCSIRDTVCATCAENSYNEMNY 67
DB 23 PYPSQAQCRNPSTBEYERLKKCKSCPPGQKAKASCSHSVDTKICPLDPTTYAMNR 82
QY 68 LRTICQLCR--PCDPMWGLIEIAPCTSKRKTKQRCQCPGFCAMLE--CTHELLSDCPPT 125
DB 83 SPQCFKCSPPCR--KQFVENQTTLSMDRICSCPENYICISKMYONCHICKVHKCGRGY 140
QY 126 ERELKQEVKGNNHCVPCKAGHFQNTSSPSARCCPHTRCENQGLVEAAPGTAQSDTTCKN 185
DB 141 RVSRRG--TSTDTTECKRCPGTFSDSESYDTSCIPHTVCKS---VAVGANNVDTVCHD 195
QY 186 PLRP-----LPPMSGT 197
DB 196 SVATALPHTAVNPLPSQSTT 216

RESULT 12
Q8K2X6 PRELIMINARY; PRT; 289 AA.
ID Q8K2X6;
AC Q8K2X6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to tumor necrosis factor receptor superfamily, member 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RA Strusberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC029254; AAH29254.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0005940; C:ribosome; IEA.
DR GO: GO:0003677; F:rRNA binding; IEA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.

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DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR GO: GO:0006412; P:protein biosynthesis; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR008063; P: receptor.
DR InterPro: IPR001005; Myb DNA binding.
DR InterPro: IPR001865; Ribosomal_S2.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR PRINTS: PR01680; FASRECEPTOR.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00037; MYB_1; 1.
DR PROSITE: PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 4.
DR Receptor.
DR SEQUENCE 289 AA; 32077 MW; DBE93B1E439F1E2A CRC64;
Query Match 21.5%; Score 243.5; DB 11; Length 289;
Best Local Similarity 31.0%; Pred. No. 2.6e-18;
Matches 54; Conservative 22; Mismatches 81; Indels 17; Gaps 5;
QY 15 TCDDQEEYEPQRIICSRCPPTVYSAKCSRIIDTVCAATCAENSYNEHNYLTICOLC 74
Db 25 TCSD--KQYHDGQ--CCDLCQPGSRILSHCTALEKTCQHPGDSGFSQAQNRIRCHQH 80
QY 75 RPPDPVWGLIEIAPCTSKRTQCRQCPQMFCAWALECTHCELLSDCPG-----TEAEI 129
Db 81 RHCEPQGLRKYKKEGTASLDIVCAKKEGQHT--SKDCEAQAQHTPLCPGQVEMMATEI 138
QY 130 KDEVKGNNHCVPCKAGHPQNTSSPSARCPHTRCENOGIYEAAPGTAGSTTC 183
Db 139 TDV-----CHPCVGFSSNQSILFEKCYFWTSCEDNLEVLQKTSQITVIC 186
RESULT 13
Q9XSZ8 PRELIMINARY; PRT; 283 AA.
AC Q9XSZ8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE HVEAS.
GN HVEAS.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=kidney;
RA MEDLINE=99296730; PubMed=10366573;
RA Foster T.P., Chouljenko V.N., Koussoulas K.G.;
RT "Functional characterization of the HveA homolog specified by African
RT green monkey kidney cells with a herpes simplex virus expressing the
RT green fluorescence protein.";
RT Virology 258:365-374(1999).
RL EMBL: AF147720; AAD37381.1; -.
DR HSSP: Q82956; LUMA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR008063; P: receptor.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR PRINTS: PR01680; FASRECEPTOR.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.

SQ SEQUENCE 283 AA; 30199 MW; 397951C6617FE3AA CRC64;
Query Match 21.4%; Score 242.5; DB 6; Length 283;
Best Local Similarity 32.2%; Pred. No. 3.3e-18;
Matches 57; Conservative 18; Mismatches 85; Indels 17; Gaps 6;
QY 9 YASENCTDQEEYEPQRIICSRCPPTVYSAKCSRIIDTVCAATCAENSYNEHNYLTICOLC 68
Db 35 YAPALPSCK--DEY--PVGSECCPKGPGFHVRAQCGEGTGVCEPSPGTIAHNGI 90
QY 69 TTCQLCRPDPVWGLIEIAPCTSKRTQCRQCPQMFCAWALECTHCELLSDCPGTEA 127
Db 91 SKCLQCQCDPAPMGLTIRNCSSTTANALCGSGFHCIIQDGHCAACRAVATSSPG----- 147
QY 128 ELKDEVKGNNH-----CVPCKAGHPQNTSSPSARCPHTRCENOGIYEAAPGTAGS 179
Db 148 ---ORVQKGSTBSQDTILCONCPPTGTF--SSNGTLEEGCHGKCKMVLTEAGPGTSSS 200
RESULT 14
Q02735 PRELIMINARY; PRT; 186 AA.
AC Q02735;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE A56R protein.
GN A56R.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RA MEDLINE=98229462; PubMed=9568042;
RA Shehelnunov S.N., Satorov P.F., Totmenin A.V., Petrov N.A.,
RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT "Species-specific differences in genome organization of cowpox,
RT smallpox and vaccinia viruses.";
RT Virology 243:432-460(1998).
RL [2]
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RA MEDLINE=97068532; PubMed=8963248;
RA Satorov P.F., Petrov N.A., Ryazankina O.I., Totmenin A.V.,
RA Shehelnunov S.N., Sandakhchiev L.S.;
RT "Genes of a circle of hosts for the cowpox virus.";
RT Dokl. Akad. Nauk 349:829-833(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RA Shehelnunov S.N., Satorov P.F., Totmenin A.V., Milyev M.V.,
RA Ryazankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J.,
RA Sandakhchiev L.S.;
RT "Structure-function and organization of cowpox virus strain GRI-90
RT complete genome.";
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=GRI-90;
RA Totmenin A.V.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL: X94355; CAD90723.1; -.
DR HSSP: Q82956; LUMA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR SEQUENCE 186 AA; 20482 MW; D2342F1040A0AEB3 CRC64;

Query Match 21.2%; Score 240; DB 12; Length 186;
 Best Local Similarity 32.2%; Pred. No. 4e-18;
 Matches 48; Conservative 25; Mismatches 66; Indels 10; Gaps 5;

QY 3 PAVAPVYASENCOTCDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENSYN 62
 DB 24 PFLPPLHAPVNSC--DEGEYLDKRHNQCNCPPGEFAKVCSGSDNTKCRCPHYT 81
 QY 63 EHMNYLTICOLCRPDPVWGLEIAPCTSKRTQCRQPMFCA--AMALECTHCELLS 119
 DB 82 AIPVNSGCHQCRKC-PTGSPDKV-KCTGTQNSKSCLPGWYCATDSSQTEPDRDVPKRS 139
 QY 120 DCPGTEALDKDEVGKNNHCVPCKAGHF 148
 DB 140 RCPGSGFGIDEG--GNPICKSCCVGEY 165

RESULT 15

Q7T2H3 PRELIMINARY; PRT; 318 AA.
 AC Q7T2H3;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Tumour necrosis factor receptor.
 GN TNFR.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_taxid=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head kidney;
 RA Zou J., Secombes C.J.;
 RT "Molecular cloning and expression analysis of a TNF receptor homologue
 in rainbow trout, *Oncorhynchus mykiss*,"
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ517804; CAD57165.1; -
 KW Receptor.
 SQ SEQUENCE 318 AA; 35254 MW; 78F8135011283B43 CRC64;

Query Match 21.1%; Score 238.5; DB 13; Length 318;
 Best Local Similarity 29.1%; Pred. No. 1e-17;
 Matches 50; Conservative 22; Mismatches 89; Indels 11; Gaps 3;

QY 16 CRDQEKYEYEPQHRICCSRCPGTYVSACSRIRDTVCATCAENSYNHMNYLTICOLCR 75
 DB 6 CKTEEYLHDASGVKRCRCRCRKGQYRTDQGSTKTECFQHEHYTAELNFKQCLPCR 65
 QY 76 PCDPVWGLEIAPCTSKRTQCRQPMFCAAMALECTHCELLSDCPPGTEALDKDEVK 135
 DB 66 VCYSNSNQVLRCECASSDRQCVCKTGYCTDGG--CEHCLPYTLCPILSGV----VWQ 118
 QY 136 GNNH---CVPKAGHFONTSSPSARCQPHTRCENOGIVEAAGTAPQSDPTTC 183
 DB 119 AMPQNDTVCAPCQPGTYNSFNDAFTHCQSHTRCGDLGKEVKSAGTETTDVAVC 170

Search completed: August 27, 2004, 21:10:26
 Job time : 120 secs

